



09-924197

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 125025

TO: Karen A Lacourciere
Location: rem/2d15/2c18
Art Unit: 1635
Monday, June 21, 2004

Case Serial Number: 09/924197

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Lacourciere,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 09:52:48 ; Search time 2214 Seconds
(without alignments)
12046.568 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagcagsgtttcccg.....tgccgattcattatgcag 5822

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgm2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgm2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgm2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 4: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 13: /cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 15: /cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgm2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgm2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgm2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5822	100.0	5822	13	US-09-924-197-1
2	2768	47.5	4773	10	US-09-991-209-32
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4	2768	47.5	4965	10	US-09-991-209-37
5	2768	47.5	4974	10	US-09-991-209-35
6	2768	47.5	5001	10	US-09-991-209-40
7	2768	47.5	5034	10	US-09-991-209-33
8	2768	47.5	5164	10	US-09-991-209-36
9	2768	47.5	5277	10	US-09-991-209-25
10	2768	47.5	5295	10	US-09-991-209-38
11	2768	47.5	5327	10	US-09-991-209-27
12	2768	47.5	5337	10	US-09-991-209-19
13	2768	47.5	5337	10	US-09-991-209-23
14	2768	47.5	5337	10	US-09-991-209-31

15	2768	47.5	5338	10	US-09-991-209-15	Sequence 15, Appl
16	2768	47.5	5338	10	US-09-991-209-29	Sequence 29, Appl
17	2768	47.5	5345	10	US-09-991-209-17	Sequence 17, Appl
18	2768	47.5	5387	10	US-09-991-209-41	Sequence 41, Appl
19	2768	47.5	5395	10	US-09-991-209-21	Sequence 21, Appl
20	2683.4	46.1	3448	15	US-10-128-590-6	Sequence 6, Appl
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22	2683.4	46.1	3448	16	US-10-128-578B-6	Sequence 6, Appl
23	2675.4	46.0	3018	13	US-09-486-142-7	Sequence 7, Appl
24	2670.2	45.9	3357	15	US-10-161-403-96	Sequence 96, Appl
25	2552	43.8	10078	14	US-10-033-190-3	Sequence 3, Appl
26	2549.4	43.8	2962	15	US-10-033-399B-10	Sequence 10, Appl
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29	2549.4	43.8	5251	14	US-10-153-159-17	Sequence 17, Appl
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32	2549	43.8	2958	15	US-10-220-262-2	Sequence 2, Appl
33	2549	43.8	2958	15	US-10-220-262-3	Sequence 3, Appl
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36	2549	43.8	4754	16	US-10-014-099F-80	Sequence 80, Appl
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38	2549	43.8	4831	16	US-10-014-099F-99	Sequence 99, Appl
39	2548.8	43.8	8858	15	US-10-378-393-1	Sequence 1, Appl
40	2538.2	43.6	10597	15	US-10-057-108-10	Sequence 10, Appl
41	2538.2	43.6	10599	15	US-10-057-108-11	Sequence 11, Appl
42	2538.2	43.6	12482	15	US-10-057-108-7	Sequence 7, Appl
43	2531.2	43.5	5175	15	US-10-057-108-6	Sequence 6, Appl
44	2531.2	43.5	8426	15	US-10-163-899-1	Sequence 1, Appl
45	2515	43.2	13910	10	US-09-919-901-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-924-197-1
; Sequence 1, Application US/09924197
; Publication No. US20030018993A1
; GENERAL INFORMATION:
; APPLICANT: Gutterson, Neal
; APPLICANT: Oeller, Paul
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
; TITLE OF INVENTION: Repeat Sequences
; FILE REFERENCE: 012176-010810US
; CURRENT APPLICATION NUMBER: US/09/924,197
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/225,508
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-924-197-1

Query Match	100.0%	Score 5822;	DB 13;	Length 5822;
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Matches 5822;	Conservative	0;		Gaps 0;
Qy	1	CTGGCAGCAGAGTTTCCGACTGGAAAGCGGCGAGTCGAGCGCAACGCAATTAATGTGAG	60	
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Qy	121	TGGATTTCTGCGCGATACCAATTTTACACAGGAACAGCTATGATGATGATGATGATG	180	
Db	121	TGGATTTCTGCGCGATACCAATTTTACACAGGAACAGCTATGATGATGATGATGATG	180	

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DB 4921 CTCATGACCAAAATCCCTTAACGTAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA 4980
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DB 5821 AG 5822

RESULT 2
US-09-991-209-32
; Sequence 32, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4773
; TPB: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pG6 vector
US-09-991-209-32

Query Match 47.5%; Score 2768; DB 10; Length 4773;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGCGTC 2894
DB 778 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGCGTC 837
QY 2895 TTGCGATGATTATCATATAATTTCTGTTGAATTAAGTAAAGCATGTAATAATTAACATGT 2954
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QY 2955 AATGCAATGCTTTTATGAGATGGTTTATGATAGTCCCGCAATTAACATTT 3014
DB 898 AATGCAATGCTTTTATGAGATGGTTTATGATAGTCCCGCAATTAACATTT 957
QY 3015 AATACCGCATAGAAAACAAAATATAGCGGCAAACTAGAGATAAATATACGCGCGGTGT 3074
DB 958 AATACCGCATAGAAAACAAAATATAGCGGCAAACTAGAGATAAATATACGCGCGGTGT 1017
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DB 1018 CATCTATGTTACTAGATTCGATAGCTTCTAGAGCGCGCGGTGGAGC-----T 1064
QY 3135 CCAATTCGCGCTATAGTGTGATTAAC---AATTCACCTGCGCGCTGTTTACACGTC 3191
DB 1065 CCAATTCGCGCTATAGTGTGATTAAC---AATTCACCTGCGCGCTGTTTACACGTC 1124
QY 3192 GTGACTGGGAAACCCCTGGCGTTTACCAACTTAATGCGCTTGACGACACATCCCTTCG 3251
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QY 5411 CCAGAGGAGAAAGCGGACAGGTATCCGTAAGCGCGAGGTCGGACAGGAGGCGCA 5470
DB 3290 CCAGAGGAGAAAGCGGACAGGTATCCGTAAGCGCGAGGTCGGACAGGAGGCGCA 3349
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DB 3350 CGAGGAGCTTCCAGGGGAGAAAGCGCTGTATCTTTATAGTCCCTGCGGTTCGCCACCC 3409
QY 5531 TCTGACTTGAGCGTCGATTTTGTGATGCTGCTCAGGGGCGGAGGCTTATGAAAAACG 5590
DB 3410 TCTGACTTGAGCGTCGATTTTGTGATGCTGCTCAGGGGCGGAGGCTTATGAAAAACG 3469
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DB 3470 CCAGCAAGCGGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTGTCTCACATGTCT 3529
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DB 3530 TTCTGCGTTATCCCTGATTCTGTGTGATAACCGTATTACCGCTTTTGTGAGTGAGTGATA 3589
QY 5711 CCCTGCGCGAGCGGACGACCGAGCGAGCGAGTCACTGAGCGAGGAGCGGAGGAGC 5770
DB 3590 CCCTGCGCGAGCGGACGACCGAGCGAGCGAGTCACTGAGCGAGGAGCGGAGGAGC 3649
QY 5771 GCCCAATACGCAACCGCTCTCCCGCGGCTTGGCGGATTCATTAATGCAG 5822
DB 3650 GCCCAATACGCAACCGCTCTCCCGCGGCTTGGCGGATTCATTAATGCAG 3701

RESULT 3
US-09-991-209-34
; Sequence 34, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991.209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 4950
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJ06.1 vector
US-09-991-209-34

Query Match 47.5%; Score 2768; DB 10; Length 4950;
Best local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AAGCAGATCGTTCAACACATTTGGCAATAAGCTTCTTAAAGATTCAATCCCTGTCGCGGTC 2894
DB 955 AAGCAGATCGTTCAACACATTTGGCAATAAGCTTCTTAAAGATTCAATCCCTGTCGCGGTC 1014
QY 2895 TTGCGATGATTATCATATAATTTCTGTGTGATTAACGTTAAGCATGTAAATAATTAACATGT 2954
DB 1015 TTGCGATGATTATCATATAATTTCTGTGTGATTAACGTTAAGCATGTAAATAATTAACATGT 1074
QY 2955 AATGCATGACGTTATTAAGATGAGGTTTATGATTAAGTCCCGCAATTAATATTAATTT 3014
DB 1075 AATGCATGACGTTATTAAGATGAGGTTTATGATTAAGTCCCGCAATTAATATTAATTT 1134
QY 3015 AATACGGGATGAGAAACAAATATAGCGCAATAGGATAGGATTAATTAATTAATTAATTT 3074
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DB 1135 AATAAGGATAGAAAAACAATAATATAGCGCGCAAACTAGGATAAATTATTCGCGCGCGGTGT 1194
QY 3075 CATCTATGTTACTAGATTCGACCTTCGAGGCAATGGAATCCGCGCGCGCAATGCGAATCGCGGC 3134
DB 1195 CATCTATGTTACTAGATTCGATAAAGCTTCTAGAGCGCGCGGTGGAGC-----T 1241
QY 3135 CCAATTCGCGCTATAGTATGATTCGTAATAGC---AATTCACATGGCGCTGTTTCAACAGTC 3191
DB 1242 CCAATTCGCGCTATAGTATGATTCGTAATAGC---AATTCACATGGCGCTGTTTCAACAGTC 1301
QY 3192 GTGACTTGGGAAAAACCCCTGGCGTTTACCCAACTTAATTCGCTTTCGAGCAATCCCTTTCG 3251
DB 1302 GTGACTTGGGAAAAACCCCTGGCGTTTACCCAACTTAATTCGCTTTCGAGCAATCCCTTTCG 1361
QY 3252 CGAGCTTGGCGTAATAGCGAAGAGGCGCGCAACCGATTCGCTTTCGCAACAGTTGCGGAGCC 3311
DB 1362 CGAGCTTGGCGTAATAGCGAAGAGGCGCGCAACCGATTCGCTTTCGCAACAGTTGCGGAGCC 1421
QY 3312 TGAATGGCGAAT--GGAGCGCGCTGTAGCGCGCATTTAAGCGCGGCGGCTGTTGTTGTTA 3370
DB 1422 TGAATGGCGAATGGAGCGCGCTGTAGCGCGCATTTAAGCGCGGCGGCTGTTGTTGTTA 1481
QY 3371 CGCGAGCGTGAACCGCTTACACTTTCGCAAGCGCGCTTTCGCTTTCGCTTTCCTTTC 3430
DB 1482 CGCGAGCGTGAACCGCTTACACTTTCGCAAGCGCGCTTTCGCTTTCGCTTTCCTTTC 1541
QY 3431 CTTCTTTTCTCGCGACGTTTCGCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTTTC 3490
DB 1542 CTTCTTTTCTCGCGACGTTTCGCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTTTC 1601
QY 3491 TAGGCTTCGATTTAGAGCTTTACGCGACCTTCGACCGCAAAACCTTGAATTTGGTGATG 3550
DB 1602 TAGGCTTCGATTTAGAGCTTTACGCGACCTTCGACCGCAAAACCTTGAATTTGGTGATG 1661
QY 3551 GTTCACGCTAGTGGCGCATCGCCCTGTAGAGCGGTTTTTCGCGCTTTCGAGCTTGAAGTCCA 3610
DB 1662 GTTCACGCTAGTGGCGCATCGCCCTGTAGAGCGGTTTTTCGCGCTTTCGAGCTTGAAGTCCA 1721
QY 3611 CGTTCCTTAATAGTGGAGCTTGTTCGCAAACTGGAACAACTCAACCTTATTCGCTTTC 3670
DB 1722 CGTTCCTTAATAGTGGAGCTTGTTCGCAAACTGGAACAACTCAACCTTATTCGCTTTC 1781
QY 3671 ATTCTTTTGTATTTATAGGAGTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCG 3730
DB 1782 ATTCTTTTGTATTTAAGGAGTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCG 1841
QY 3731 TTTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTTTCGCTTTCGATG 3790
DB 1842 TTTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTTTCGCTTTCGATG 1892
QY 3791 CGGTAATTTCTCTTACGCAATCTGTCGCGGTAATTTTCAACCGCATACAGGTCGCTTTC 3850
DB 1893 -----AGTGGCGACTTTTC 1906
QY 3851 GGGGAAATGCGCGGAACCCCTATTTGTTTATTTTCTTAATATACATTTCAATATGATTC 3910
DB 1907 GGGGAAATGCGCGGAACCCCTATTTGTTTATTTTCTTAATATACATTTCAATATGATTC 1966
QY 3911 CGCTCATGAGCAATAACCTCTGATAAATGCTTCAATAATATTTGAAAAAGGAGGATGA 3970
DB 1967 CGCTCATGAGCAATAACCTCTGATAAATGCTTCAATAATATTTGAAAAAGGAGGATGA 2026
QY 3971 GTATTCAAATTTCCGTCGCGCTTATTCCTTTTTCGCGCAATTTTCGCTTTCGCTTTC 4030
DB 2027 GTATTCAAATTTCCGTCGCGCTTATTCCTTTTTCGCGCAATTTTCGCTTTCGCTTTC 2086
QY 4031 TTGCTCAACCCAGAAACCTGCTGGAAGTAAAGATGCTGAGGTCAGTTGGTGCACGAG 4090
DB 2087 TTGCTCAACCCAGAAACCTGCTGGAAGTAAAGATGCTGAGGTCAGTTGGTGCACGAG 2146
QY 4091 TGGGTTACATCGAATCTGATCTCAACAGCGGTAAGATCTTTGAGAGTTTTCGCGCGGAG 4150
DB 2147 TGGGTTACATCGAATCTGATCTCAACAGCGGTAAGATCTTTGAGAGTTTTCGCGCGGAG 2206
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QY 4151 AACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATATGTGGCGGGTATTAATCCCGTA 4210
Db 2207 AACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATATGTGGCGGGTATTAATCCCGTA 2266
QY 4211 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATCTCTCAGAAATGACTTGGTTG 4270
Db 2267 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATCTCTCAGAAATGACTTGGTTG 2326
QY 4271 AGTACTCACAGTCACAGAAAGCACTTAAGGATGCGCATGACAGTAAGAGAAATATGCA 4330
Db 2327 AGTACTCACAGTCACAGAAAGCACTTAAGGATGCGCATGACAGTAAGAGAAATATGCA 2386
QY 4331 GTGCTGCATAAACATGAGTGATAACTCTGGGCAACTTACTTCTGACAAACGATCGGAG 4390
Db 2387 GTGCTGCATAAACATGAGTGATAACTCTGGGCAACTTACTTCTGACAAACGATCGGAG 2446
QY 4391 GACCGAAGGAGCTAACCGCTTTTTCACAAACATGGGGGATCAATGTAACCTGCGCTTGATC 4450
Db 2447 GACCGAAGGAGCTAACCGCTTTTTCACAAACATGGGGGATCAATGTAACCTGCGCTTGATC 2506
QY 4451 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACACGATGCGCTG 4510
Db 2507 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACACGATGCGCTG 2566
QY 4511 TAGCAATGGCAACAACTGTCGCAAACTATTAACCTGGCGAACTACTTCTAGCTTCCC 4570
Db 2567 TAGCAATGGCAACAACTGTCGCAAACTATTAACCTGGCGAACTACTTCTAGCTTCCC 2626
QY 4571 GGCACAAATTAATAGCTGATGGAGCGGATTAAGTTGACGACCACTTCTGGCTCGG 4630
Db 2627 GGCACAAATTAATAGCTGATGGAGCGGATTAAGTTGACGACCACTTCTGGCTCGG 2686
QY 4631 CCCTTCGGGCTGGCTGTTATGCTCATAAATCTGGAGCGGTGAGCGGTGCTCGCG 4690
Db 2687 CCCTTCGGGCTGGCTGTTATGCTCATAAATCTGGAGCGGTGAGCGGTGCTCGCG 2746
QY 4691 GTATCATTTGACGACTGGGCGAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA 4750
Db 2747 GTATCATTTGACGACTGGGCGAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA 2806
QY 4751 CGGGAGTCAGGCACACTATGGATGAACGAATAGACAGATCGCTGACATAGGTGCTCAC 4810
Db 2807 CGGGAGTCAGGCACACTATGGATGAACGAATAGACAGATCGCTGACATAGGTGCTCAC 2866
QY 4811 TGATTAAGCAATGGTAAGTCTGACACCAAGTTTACTCATATATCTTTAGATTGAATTA 4870
Db 2867 TGATTAAGCAATGGTAAGTCTGACACCAAGTTTACTCATATATCTTTAGATTGAATTA 2926
QY 4871 AACTTCATTTTAAATTAAGGATCTAGGTGAAGATCCCTTTTGTGATAATCTCATGACCA 4930
Db 2927 AACTTCATTTTAAATTAAGGATCTAGGTGAAGATCCCTTTTGTGATAATCTCATGACCA 2986
QY 4931 AATCCCTTAACGTAGTTTCTGTCACCTGAGCGGTGAGCCCGGTAGAAAGATCAAG 4990
Db 2987 AATCCCTTAACGTAGTTTCTGTCACCTGAGCGGTGAGCCCGGTAGAAAGATCAAG 3046
QY 4991 GATCTTCTTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTGTCGCAACAAAAACCA 5050
Db 3047 GATCTTCTTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTGTCGCAACAAAAACCA 3106
QY 5051 CGCTACAGCGGTGTTGTTTGGGATCAAGAGCTACCACTCTTTTCCGAAAGTAA 5110
Db 3107 CGCTACAGCGGTGTTGTTTGGGATCAAGAGCTACCACTCTTTTCCGAAAGTAA 3166
QY 5111 CTGCTTTCAGCAGCGCATACCAATCTGTTCTAGTGTAGCGGTAGTTAGGCC 5170
Db 3167 CTGCTTTCAGCAGCGCATACCAATCTGTTCTAGTGTAGCGGTAGTTAGGCC 3226
QY 5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTAGCAG 5230
Db 3227 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTAGCAG 3286
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QY 5231 TGCTGTGCTCCAGTGGGATAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 5290
Db 3287 TGCTGTGCTCCAGTGGGATAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 3346
QY 5291 CGGATAAGGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGCCCAAGCTTGGAGC 5350
Db 3347 CGGATAAGGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGCCCAAGCTTGGAGC 3406
QY 5351 GAACGACCTACACCGAACTGAGATACCTACAGCTGAGCTATGAGAAAGCGCCAGCTTC 5410
Db 3407 GAACGACCTACACCGAACTGAGATACCTACAGCTGAGCTATGAGAAAGCGCCAGCTTC 3466
QY 5411 CCGAAGGAGAAAGCGGACAGCTATCGGTAAAGCGGCGGTGGACAGAGCGCA 5470
Db 3467 CCGAAGGAGAAAGCGGACAGCTATCGGTAAAGCGGCGGTGGACAGAGCGCA 3526
QY 5471 CGAGGAGCTTTCAGAGGCGAAACCGCTGGTATCTTTATAGTCTCTGTCGGGTTTCCGCCACC 5530
Db 3527 CGAGGAGCTTTCAGAGGCGAAACCGCTGGTATCTTTATAGTCTCTGTCGGGTTTCCGCCACC 3586
QY 5531 TCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAAGGGGGCGGAGCCTATGGAACAAACG 5590
Db 3587 TCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAAGGGGGCGGAGCCTATGGAACAAACG 3646
QY 5591 CCAGCAACCGGCTTTTAAAGGTTCTGCGCTTTTCTGCGCTTTTCTGCTCAGATGTTCT 5650
Db 3647 CCAGCAACCGGCTTTTAAAGGTTCTGCGCTTTTCTGCGCTTTTCTGCTCAGATGTTCT 3706
QY 5651 TTCTGCGTTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCTTTTGTAGTGAGCTGATA 5710
Db 3707 TTCTGCGTTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCTTTTGTAGTGAGCTGATA 3766
QY 5711 CCGCTCCCGCAGCGCAACCGACCGAGCGCAGAGCTCAGTGAGCGAGGAGGAGGAGC 5770
Db 3767 CCGCTCCCGCAGCGCAACCGACCGAGCGCAGAGCTCAGTGAGCGAGGAGGAGGAGC 3826
QY 5771 GCCCAATACGCAACCGCTCTCCCGCGGTGGCGGATTCATTAATGCGAG 5822
Db 3827 GCCCAATACGCAACCGCTCTCCCGCGGTGGCGGATTCATTAATGCGAG 3878

RESULT 4
; Sequence 37, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJQ3 vector
US-09-991-209-37

Query Match 47.5%; Score 2768; DB 10; Length 4965;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AAGCAGATCGTTCAAAATTTGGCAATTAAGTTTCTTAAGATTCGAATCTGTTGCGGTC 2894
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Db 1824 AAGCAGATCGTTCAACCAATTTGGCAATAAAGTTCTTTAAGATTGAATCCTGTTGCCGGTC 1883
Qy 2895 TTGGGATGATATCATATAATTTCTGTGTGAATTAAGTATGATTAATTAATTAACATGT 2954
Db 1884 TTGGGATGATATCATATAATTTCTGTGTGAATTAAGTATGATTAATTAATTAACATGT 1943
Qy 2955 AATGCAATGAGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTAACATTT 3014
Db 1944 AATGCAATGAGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTAACATTT 2003
Qy 3015 AATACCGGATAGAAAACAAATAATAGCGCAAACTAGGATAAATTAATCGCGCGGTGT 3074
Db 2004 AATACCGGATAGAAAACAAATAATAGCGCAAACTAGGATAAATTAATCGCGCGGTGT 2063
Qy 3075 CATCTATGTTACTAGATCGACTGCGAGGCAATGGATCCGCGCGGCAATGCGATCGCGGC 3134
Db 2064 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGGAGC-----T 2110
Qy 3135 CCAATTGCGCCTATAGTAGAGTCGTATTAG--AATTCACTGGCGCTGTTTAAACAGTC 3191
Db 2111 CCAATTGCGCCTATAGTAGAGTCGTATTAGCGGCGCTCACTGGCGCTGTTTAAACAGTC 2170
Qy 3192 GTGACTGGGAAAACCCCTGGGTTTACCCAACTTAATCGCCTTGCGAGCAATCCGCCCTTTCG 3251
Db 2171 GTGACTGGGAAAACCCCTGGGTTTACCCAACTTAATCGCCTTGCGAGCAATCCGCCCTTTCG 2230
Qy 3252 CCAAGTGGCGTAATAGCGAAGAGGCCCGCAACCGATCGCCTTCCCAACAGTTGGCGAGCC 3311
Db 2231 CCAAGTGGCGTAATAGCGAAGAGGCCCGCAACCGATCGCCTTCCCAACAGTTGGCGAGCC 2290
Qy 3312 TGAATGCGCAAT--GGAGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGCGGTGA 3370
Db 2291 TGAATGCGCAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGCGGTGA 2350
Qy 3371 CGCGCAGCGTGAACGCTTACACTTGGCAGCGCCCTAGCGCGGCTTCCCTTTCGCTTTC 3430
Db 2351 CGCGCAGCGTGAACGCTTACACTTGGCAGCGCCCTAGCGCGGCTTCCCTTTCGCTTTC 2410
Qy 3431 CTTTCCTTTCTCGCAGCTTTCGCGGCTTTCGCGTCAAGCTCTAAATCGGGGCTCGCTT 3490
Db 2411 CTTTCCTTTCTCGCAGCTTTCGCGGCTTTCGCGTCAAGCTCTAAATCGGGGCTCGCTT 2470
Qy 3491 TAGGGTTCCGATTTAGAGCTTTACGCGACCTCGACCGCAAAACTTTGATTGGGTGATG 3550
Db 2471 TAGGGTTCCGATTTAGTGTCTTTAGCGCACCTCGACCCCAAAACTTTGATTAGGGTGTG 2530
Qy 3551 GTTCAGCTAGTGGGCCATCGCCCTGTATAGACGGTTTTTCGCCCTTTTGAAGCTTGGAGTCCA 3610
Db 2531 GTTCAGCTAGTGGGCCATCGCCCTGTATAGACGGTTTTTCGCCCTTTTGAAGCTTGGAGTCCA 2590
Qy 3611 CGTTCTTTAATAGTGGACTCTGTTCGCAACTGGACCAACACTCAACCCCTATCTCGGTCT 3670
Db 2591 CGTTCTTTAATAGTGGACTCTGTTCGCAACTGGACCAACACTCAACCCCTATCTCGGTCT 2650
Qy 3671 ATTCTTTTGAATTTAAGGATTTTCGCGATTTTCGCGCTATTCGTTTAAATAATAGCTGA 3730
Db 2651 ATTCTTTTGAATTTAAGGATTTTCGCGATTTTCGCGCTATTCGTTTAAATAATAGCTGA 2710
Qy 3731 TTTTAAACAAATTAATTAACGCGAAATTTTAAACAAATATTAACGTTTACAAATTTTCGCTGATG 3790
Db 2711 TTTTAAACAAATTTTAAACGCGAAATTTTAAACAAATATTAACGTTTACAAATTT 2761
Qy 3791 CGGTATTTCTCCTTACGCACTGTGGCGATTTCACACCGCATACAGGTGGCACTTTTC 3850
Db 2762 -----AGGTGGCACTTTTC 2775
Qy 3851 GGGGAAATGCGCGAACCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATC 3910
Db 2776 GGGGAAATGCGCGAACCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATC 2835
Qy 3911 CGCTCATGAGCAATAACCTCGATAAATGCTTCAATAATTTGAAAGAGGAGATGA 3970
Db 2836 CGCTCATGAGCAATAACCTCGATAAATGCTTCAATAATTTGAAAGAGGAGATGA 2895

Qy 3971 GTATTCAACATTTCCGTTGCTCGCCCTTAATTCCTTTTTTTTGGGCAATTTTGCCTTCTCTGTTT 4030
Db 2896 GTATTCAACATTTCCGTTGCTCGCCCTTAATTCCTTTTTTTTGGGCAATTTTGCCTTCTCTGTTT 2955
Qy 4031 TTGCTCACCCAGAAAAACGCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACACGAG 4090
Db 2956 TTGCTCACCCAGAAAAACGCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACACGAG 3015
Qy 4091 TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAAGTCTTTCGCCCCGAG 4150
Db 3016 TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAAGTCTTTCGCCCCGAG 3075
Qy 4151 AAGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTTGGCGGCTATTATCCCGTA 4210
Db 3076 AAGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGTTGGCGGCTATTATCCCGTA 3135
Qy 4211 TTCAACGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAAATGACTTGGTTG 4270
Db 3136 TTCAACGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAAATGACTTGGTTG 3195
Qy 4271 AGTACTCACCACTCAAGAAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTAAGCA 4330
Db 3196 AGTACTCACCACTCAAGAAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTAAGCA 3255
Qy 4331 GTGCTGCGCATAAACATGAGTGATTAACACTGCGGCCAACTTACTTCTGACAAAGATCGGAG 4390
Db 3256 GTGCTGCGCATAAACATGAGTGATTAACACTGCGGCCAACTTACTTCTGACAAAGATCGGAG 3315
Qy 4391 GACCGAAGAGAGCTTAAACCGCTTTTTTGCAACAATGGGGGATCATGTAACTCGCCTTGATC 4450
Db 3316 GACCGAAGAGAGCTTAAACCGCTTTTTTGCAACAATGGGGGATCATGTAACTCGCCTTGATC 3375
Qy 4451 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAAACGAGCGGTGACACCAAGATGCGCTG 4510
Db 3376 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAAACGAGCGGTGACACCAAGATGCGCTG 3435
Qy 4511 TAGCAATGGCAACAAAGCTTTCGCAAACTATTAACTGCGCAACTTACTTCTAGCTTCTCC 4570
Db 3436 TAGCAATGGCAACAAAGCTTTCGCAAACTATTAACTGCGCAAACTTACTTCTAGCTTCTCC 3495
Qy 4571 GGCAACAATTAATAGATCTGGATGGAGCGGATAAAGTTGCGAGGACCACTTCTGCGCTCGG 4630
Db 3496 GGCAACAATTAATAGATCTGGATGGAGCGGATAAAGTTGCGAGGACCACTTCTGCGCTCGG 3555
Qy 4631 CCCTTCGCGCTGCGTGGTTTATTTGCTGATTAATCTGAGCGCGGTGAGCGTGGGTCTCGCG 4690
Db 3556 CCCTTCGCGCTGCGTGGTTTATTTGCTGATTAATCTGAGCGCGGTGAGCGTGGGTCTCGCG 3615
Qy 4691 GTATCATTTGCGACACTGGGSCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA 4750
Db 3616 GTATCATTTGCGACACTGGGSCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA 3675
Qy 4751 CGGGGAGTCAGGCAACTATGATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTCAC 4810
Db 3676 CGGGGAGTCAGGCAACTATGATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTCAC 3735
Qy 4811 TGATTAAGCAATTTGGTTAACTGCTGAGCAACCAAGTTTACTCATATATCTTTAGATTGATTAA 4870
Db 3736 TGATTAAGCAATTTGGTTAACTGCTGAGCAACCAAGTTTACTCATATATCTTTAGATTGATTAA 3795
Qy 4871 AACTTCATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTTTTGTATAATCTCATGACCA 4930
Db 3796 AACTTCATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTTTTGTATAATCTCATGACCA 3855
Qy 4931 AAATCCCTTAAACGCTGAGTTTTCGTTCCACTGAGCGGTGAGACCCCGGTAGAAAAGATCAAAG 4990
Db 3856 AAATCCCTTAAACGCTGAGTTTTCGTTCCACTGAGCGGTGAGACCCCGGTAGAAAAGATCAAAG 3915
Qy 4991 GATCTCTTGGAGATCCTTTTTTCTGCGCGGTAACTGCTGCTTGCCTGCAAAACAAAAACAC 5050
Db 3916 GATCTCTTGGAGATCCTTTTTTCTGCGCGGTAACTGCTGCTTGCCTGCAAAACAAAAACAC 3975

QY 3791 CGGTATTTTCTCCTTACGCATCTGCGCGGTATTTTCAACCGCATACAGGTGGCACTTTTC 3850
DB 2771 -----AGGTGGCACTTTTC 2784
QY 3851 GGGAAATGTGCGGGAACCCCTATTATTTGTTTATTTTCTAAATACATTTCAAAATATGATC 3910
DB 2785 GGGAAATGTGCGGGAACCCCTATTATTTGTTTATTTTCTAAATACATTTCAAAATATGATC 2844
QY 3911 CGCTCATGAGACAATAAACCTCTGATAAATGCTTCAATATATTTGAAAAAGGAAGATAGA 3970
DB 2845 CGCTCATGAGACAATAAACCTCTGATAAATGCTTCAATATATTTGAAAAAGGAAGATAGA 2904
QY 3971 GTATTCAACATTTTCCGTTGTCGCCCTTATTCCTTTTGTGGGCAATTTTGCCTTCTGTTT 4030
DB 2905 GTATTCAACATTTTCCGTTGTCGCCCTTATTCCTTTTGTGGGCAATTTTGCCTTCTGTTT 2964
QY 4031 TTGCTCACCCAGAAACCTGCTGTAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 4090
DB 2965 TTGCTCACCCAGAAACCTGCTGTAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 3024
QY 4091 TGGGTTACATCGAATCGAATCTCAACAGCGGTAAAGATCTTGAAGATTTTTCGCCCGGAAG 4150
DB 3025 TGGGTTACATCGAATCGAATCTCAACAGCGGTAAAGATCTTGAAGATTTTTCGCCCGGAAG 3084
QY 4151 AACGTTTTCGAATGATGACACTTTTAAAGTTCTGCTATGTTGGCGGGTATTATTCGGTA 4210
DB 3085 AACGTTTTCGAATGATGACACTTTTAAAGTTCTGCTATGTTGGCGGGTATTATTCGGTA 3144
QY 4211 TTGACGCGGGCAAGAGCACTCGTCCGCGCATACACTATTCTCAGAATGACTTGGTGG 4270
DB 3145 TTGACGCGGGCAAGAGCACTCGTCCGCGCATACACTATTCTCAGAATGACTTGGTGG 3204
QY 4271 AGTACTCACGATCACAGAAAAGCATCTTACGATGGCATGACAGTAAGAAGATTAATGCA 4330
DB 3205 AGTACTCACGATCACAGAAAAGCATCTTACGATGGCATGACAGTAAGAAGATTAATGCA 3264
QY 4331 GTCTCTGCCATAACCATGAGTGAACACTTGGGCGCACTTACTTCTGACGAACGATCGGAG 4390
DB 3265 GTCTCTGCCATAACCATGAGTGAACACTTGGGCGCACTTACTTCTGACGAACGATCGGAG 3324
QY 4391 GACCGAAGGAGCTAAACCGCTTTTGTGCAACAATGCGGATCATGTAACTCGCTTGATC 4450
DB 3325 GACCGAAGGAGCTAAACCGCTTTTGTGCAACAATGCGGATCATGTAACTCGCTTGATC 3384
QY 4451 GTTGGAAACCGGAGCTGAATGAAGCCATACCAAACGACGCTGACACCAAGATGCTG 4510
DB 3385 GTTGGAAACCGGAGCTGAATGAAGCCATACCAAACGACGCTGACACCAAGATGCTG 3444
QY 4511 TAGCAATGGCAACAACTGTCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCC 4570
DB 3445 TAGCAATGGCAACAACTGTCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCC 3504
QY 4571 GGCACAAATTAATAGACTGGAGCGGATAAAGTTGACGACCACTTCTGCGCTGG 4630
DB 3505 GGCACAAATTAATAGACTGGAGCGGATAAAGTTGACGACCACTTCTGCGCTGG 3564
QY 4631 CCCTTCGGCTGCTGTTTATTTGCTGATAAATCTGAGACCGGTGAGCGGTCTCGG 4690
DB 3565 CCCTTCGGCTGCTGTTTATTTGCTGATAAATCTGAGACCGGTGAGCGGTCTCGG 3624
QY 4691 GTATCATTTGACGACTTGGGCGCAGATGTTAAGCCCTCCGATCGTAGTTATCTACAOGA 4750
DB 3625 GTATCATTTGACGACTTGGGCGCAGATGTTAAGCCCTCCGATCGTAGTTATCTACAOGA 3684
QY 4751 CGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTTCAC 4810
DB 3685 CGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTTCAC 3744
QY 4811 TGATTAAGCAATTGGTAACTGTGACAGCAAGTTTACTCATATATCTTTAGATTTGATTA 4870
DB 3745 TGATTAAGCAATTGGTAACTGTGACAGCAAGTTTACTCATATATCTTTAGATTTGATTA 3804

QY 4871 AACTTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGTATATCTCATGACCA 4930
DB 3805 AACTTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGTATATCTCATGACCA 3864
QY 4931 AAATCCCTTAAACGTAGTGTTCCTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAG 4990
DB 3865 AAATCCCTTAAACGTAGTGTTCCTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAG 3924
QY 4991 GATCTTCTGAGATCCCTTTTTCCTGCGGTAAATCTGCTGTGCTTGCAAAACAAAAACCAAC 5050
DB 3925 GATCTTCTGAGATCCCTTTTTCCTGCGGTAAATCTGCTGTGCTTGCAAAACAAAAACCAAC 3984
QY 5051 CGCTTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAACTCTTTTTCGCGAGGTAA 5110
DB 3985 CGCTTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAACTCTTTTTCGCGAGGTAA 4044
QY 5111 CTGCTTTCAGCAGAGCGCAGATACAAATACCTGCTTCTAGTGTAGCCGTAGTTAGGCC 5170
DB 4045 CTGCTTTCAGCAGAGCGCAGATACCAATACCTGCTTCTAGTGTAGCCGTAGTTAGGCC 4104
QY 5171 ACCACTTCAAGAACTCTGTAGCACCGCTCATATACCTGCTCTGCTAATCTGTTACCAG 5230
DB 4105 ACCACTTCAAGAACTCTGTAGCACCGCTCATATACCTGCTCTGCTAATCTGTTACCAG 4164
QY 5231 TGGCTGCTGCGAGTGGCGATAGTGTCTTACCGGGTGGACTCAAGACGATAGTTAC 5290
DB 4165 TGGCTGCTGCGAGTGGCGATAGTGTCTTACCGGGTGGACTCAAGACGATAGTTAC 4224
QY 5291 CGGATAAGCGCGCAGCGCTCGGGCTGAACCGGGGTTCGTGACACAGCCAGCTTGGAGC 5350
DB 4225 CGGATAAGCGCGCAGCGCTCGGGCTGAACCGGGGTTCGTGACACAGCCAGCTTGGAGC 4284
QY 5351 GAACGACTTACACCGAACTGAGATACCTACAGCGTGAATATGAGAAAGCCGCTTC 5410
DB 4285 GAACGACTTACACCGAACTGAGATACCTACAGCGTGAATATGAGAAAGCCGCTTC 4344
QY 5411 CCGAAGGAGAAAGCGGACAGGTATCCGCTAGCGGCGAGGTGCGAACAGAGAGCGCA 5470
DB 4345 CCGAAGGAGAAAGCGGACAGGTATCCGCTAGCGGCGAGGTGCGAACAGAGAGCGCA 4404
QY 5471 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTGCTCGGGTTTCGCCACC 5530
DB 4405 CGAGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTGCTCGGGTTTCGCCACC 4464
QY 5531 TCTGACTTGAGCGTTCGATTTTGTGATGCTGCTCAGGGGGCGGAGCTATGGAANAACG 5590
DB 4465 TCTGACTTGAGCGTTCGATTTTGTGATGCTGCTCAGGGGGCGGAGCTATGGAANAACG 4524
QY 5591 CCAGCAACGCGCTTTTTCAGCGTTCTGCGCTTTTGTGCTGCGCTTTTGTGCTGCTGCT 5650
DB 4525 CCAGCAACGCGCTTTTTCAGCGTTCTGCGCTTTTGTGCTGCGCTTTTGTGCTGCTGCT 4584
QY 5651 TTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTTACCGCTTTTGTGCTGCTGCTGATA 5710
DB 4585 TTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTTACCGCTTTTGTGCTGCTGATA 4644
QY 5711 CCCTGCGCGCAGCGCAACGACCGAGCGCAGCGAGTCAGTGAAGCGAGCGGAGAGC 5770
DB 4645 CCCTGCGCGCAGCGCAACGACCGAGCGCAGCGAGTCAGTGAAGCGAGCGGAGAGC 4704
QY 5771 GCCCAATAGCAAAACCGCTTCTCCCGCGCTTGGCGGATTCATTAAATGCAAG 5822
DB 4705 GCCCAATAGCAAAACCGCTTCTCCCGCGCTTGGCGGATTCATTAAATGCAAG 4756

RESULT 6

US-09-991-209-40
; Sequence 40, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip

;; TITLE OF INVENTION: Manipulation of the Phenolic Acid
;; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
;; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
;; FILE REFERENCE: GC648-2
;; CURRENT APPLICATION NUMBER: US/09/991,209
;; CURRENT FILING DATE: 2002-07-02
;; PRIOR APPLICATION NUMBER: US 60/249,608
;; PRIOR FILING DATE: 2000-11-17
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 40
;; LENGTH: 5001
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: pub8.11 vector
;; FEATURE:
;; NAME/KEY: misc.feature
;; LOCATION: (1)...(5001)
;; OTHER INFORMATION: n = A,T,C or G
US-09-991-209-40

Query Match 47.5%; Score 2768; DB 10; Length 5001;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTTGAATCCTGTGCGGTC 2894
Db |||||
Qy 1856 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTTGAATCCTGTGCGGTC 1915
Db |||||
Qy 2895 TTGGATGATTTATCATATAATTTCTGTGAATAGTTTAAAGATGTAATTAATTAACATGT 2954
Db |||||
Qy 1916 TTGGATGATTTATCATATAATTTCTGTGAATAGTTTAAAGATGTAATTAATTAACATGT 1975
Db |||||
Qy 2955 AATCATGACGTTATTTATGAGATGGTTTATGATTTAGATTCGCGCAATTTATACATTT 3014
Db |||||
Qy 1976 AATCATGACGTTATTTATGAGATGGTTTATGATTTAGATTCGCGCAATTTATACATTT 2035
Db |||||
Qy 3015 AATACGGATAGAAACAAATATAGCGCGAACTAGGATAAATTTATCGCGCGGTGT 3074
Db |||||
Qy 2036 AATACGGATAGAAACAAATATAGCGCGAACTAGGATAAATTTATCGCGCGGTGT 2095
Db |||||
Qy 3075 CATCTATGTTACTAGATCGACTCGAGGCATGGATCGCGCGCGCATGCGACGTGCGGC 3134
Db |||||
Qy 2096 CATCTATGTTACTAGATCGATTAAGCTTCTAGAGCGCGGTGGAGC-----T 2142
Db |||||
Qy 3135 CCAATTCGCTTATAGTGAGTCTGTTATAC-----AATTCATCGCGCTGTTTATACAGCTC 3191
Db |||||
Qy 2143 CCAATTCGCTTATAGTGAGTCTGTTATAGCGCGCTCTACTGCGCGTCTGTTTATACAGCTC 2202
Db |||||
Qy 3192 GTGACTGGGAAACCTTGGCGTTACCCAACTTAATGCGCTTTGCGACATCCCCCTTTTCG 3251
Db |||||
Qy 2203 GTGACTGGGAAACCTTGGCGTTACCCAACTTAATGCGCTTTGCGACATCCCCCTTTTCG 2262
Db |||||
Qy 3252 CCAGCTGGGTAATAGCGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGCGAGCC 3311
Db |||||
Qy 2263 CCAGCTGGGTAATAGCGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGCGAGCC 2322
Db |||||
Qy 3312 TGAATGCGGAAT -GGAGCGCCCTGTAGCGCGGATTAAGCGCGCGGTGTTGTTGTTA 3370
Db |||||
Qy 2323 TGAATGCGGAATGGAACGCGCCCTGTAGCGCGGATTAAGCGCGCGGTGTTGTTGTTA 2382
Db |||||
Qy 3371 CGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCGCTCTTTTCGCTTTCTTC 3430
Db |||||
Qy 2383 CGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCGCGCTCTTTTCGCTTTCTTC 2442
Db |||||
Qy 3431 CTTCTTTCTCGCAAGTTTCGCGCGCTTTTCCTCGCTCAAGCTCTAAATCGGGGCTTCCCTT 3490
Db |||||
Qy 2443 CTTCTTTCTCGCAAGTTTCGCGCGCTTTTCCTCGCTCAAGCTCTAAATCGGGGCTTCCCTT 2502
Db |||||
Qy 3491 TAGGGTTCCGATTTAGAGCTTTAGGCACTTCGACCGCAAAACTTGAATTTGGGTGATG 3550
Db |||||
Qy 2503 TAGGGTTCCGATTTAGTGTCTTTAGGCACTTCGACCGCAAAACTTGAATTTAGGGTGTATG 2562
Db |||||

Qy 3551 GTTCAAGTAGTGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCA 3610
Db |||||
Qy 2563 GTTCAAGTAGTGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCA 2622
Db |||||
Qy 3611 GGTCTCTTAATAGTGGACTCTGTTCCTCAACCTGGAAACAACTCAACCTCTATCTCGGTCT 3670
Db |||||
Qy 2623 GGTCTCTTAATAGTGGACTCTGTTCCTCAACCTGGAAACAACTCAACCTCTATCTCGGTCT 2682
Db |||||
Qy 3671 ATTCTTTTGAATTTAATAGGGAATTTTCGCGATTTTCGCGCTTATGGTTAAATAAATGAGCTGA 3730
Db |||||
Qy 2683 ATTCTTTTGAATTTAATAGGGAATTTTCGCGATTTTCGCGCTTATGGTTAAATAAATGAGCTGA 2742
Db |||||
Qy 3731 TTTAAACAAATATTTAAACCGGAATTTTAAACAAATATTTAAACGTTTACAAATTTCCGCTGATG 3790
Db |||||
Qy 2743 TTTAAACAAATATTTAAACCGGAATTTTAAACAAATATTTAAACGTTTACAAATTT----- 2793
Db |||||
Qy 3791 CGGTATTTTCTCTTAAOCATCTGTGCGGTATTTTACACCGCATACAGGTGGCAGCTTTTTC 3850
Db |||||
Qy 2794 -----AGGTGGCAGCTTTTTC 2807
Db |||||
Qy 3851 GGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGTATC 3910
Db |||||
Qy 2808 GGGGAAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGTATC 2867
Db |||||
Qy 3911 CGCTCATGAGCAATAAACCTCTGATTAATGCTTCAATAATATTTGAAAGGAAGAGATGA 3970
Db |||||
Qy 2868 CGCTCATGAGCAATAAACCTCTGATTAATGCTTCAATAATATTTGAAAGGAAGAGATGA 2927
Db |||||
Qy 3971 GTATTTCAACATTTCCGTGTGCGCTTATTCCTTTTTCGCGCATTTTTCCTTTTTCCTTTT 4030
Db |||||
Qy 2928 GTATTTCAACATTTCCGTGTGCGCTTATTCCTTTTTCGCGCATTTTTCCTTTTTCCTTTT 2987
Db |||||
Qy 4031 TTGCTCACCAGAAACGCTGTGTAAGATGCTGAAGATCAGTTGGGTGGACGAG 4090
Db |||||
Qy 2988 TTGCTCACCAGAAACGCTGTGTAAGATGCTGAAGATCAGTTGGGTGGACGAG 3047
Db |||||
Qy 4091 TGGGTTACATCGAATCGAATCTCAACAGCGGTGAAGATCTTTGAGAGTTTTCGCCCGGAG 4150
Db |||||
Qy 3048 TGGGTTACATCGAATCGAATCTCAACAGCGGTGAAGATCTTTGAGAGTTTTCGCCCGGAG 3107
Db |||||
Qy 4151 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTCGCGGTATTTATCCGTA 4210
Db |||||
Qy 3108 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTCGCGGTATTTATCCGTA 3167
Db |||||
Qy 4211 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGATCTGGTTG 4270
Db |||||
Qy 3168 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGATCTGGTTG 3227
Db |||||
Qy 4271 AGTACTCACCAGTCAAGAAAGCACTTTAGCGATGGCATGACAGTAAAGAAATTTATGCA 4330
Db |||||
Qy 3228 AGTACTCACCAGTCAAGAAAGCACTTTAGCGATGGCATGACAGTAAAGAAATTTATGCA 3287
Db |||||
Qy 4331 GTGCTGCGCATTAACCACTGATGATTAACCTGCGGCAACTTCTCTGCAACAGTGGAG 4390
Db |||||
Qy 3288 GTGCTGCGCATTAACCACTGATGATTAACCTGCGGCAACTTCTCTGCAACAGTGGAG 3347
Db |||||
Qy 4391 GACCGAAGGAGCTAAACCGCTTTTTCGCAACATGGGGGATCATGTAACTCGCTTGTATC 4450
Db |||||
Qy 3348 GACCGAAGGAGCTAAACCGCTTTTTCGCAACATGGGGGATCATGTAACTCGCTTGTATC 3407
Db |||||
Qy 4451 GTTGGGAAACCGGAGCTGAATGAAGCATACCAACGAGCGGGTGAACCAAGATGCGCTG 4510
Db |||||
Qy 3408 GTTGGGAAACCGGAGCTGAATGAAGCATACCAACGAGCGGGTGAACCAAGATGCGCTG 3467
Db |||||
Qy 4511 TAGCAATGGCAACAGCTTGGCGCAACTTATTAACCTGGCGAACTACTTCTCTAGCTTCC 4570
Db |||||
Qy 3468 TAGCAATGGCAACAGCTTGGCGCAACTTATTAACCTGGCGAACTACTTCTCTAGCTTCC 3527
Db |||||
Qy 4571 GGCACAAATTAATAGATGGAATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGG 4630
Db |||||
Qy 3528 GGCACAAATTAATAGATGGAATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGG 3587
Db |||||

QY 4631 CCCTTCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGCTGAGCGTGGGTCTCGCG 4690
DB 3588 CCCTTCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGCTGAGCGTGGGTCTCGCG 3647
QY 4691 GTATCATGTGAGCACTGGGCGCAGATGCTAAGCCCTCCCGTATGCTAGTTATCTACACGA 4750
DB 3648 GTATCATGTGAGCACTGGGCGCAGATGCTAAGCCCTCCCGTATGCTAGTTATCTACACGA 3707
QY 4751 CGGGAGTACGGCACTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCCTCAC 4810
DB 3708 CGGGAGTACGGCACTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCCTCAC 3767
QY 4811 TGATTAAGCACTGGTAACTCTCAGACCAAGTTTACTCATATATATCTTTAGATGATTTAA 4870
DB 3768 TGATTAAGCACTGGTAACTCTCAGACCAAGTTTACTCATATATATCTTTAGATGATTTAA 3827
QY 4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGATATCTCATGACCA 4930
DB 3828 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGATATCTCATGACCA 3887
QY 4931 AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAAG 4990
DB 3888 AAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAGATCAAAG 3947
QY 4991 GATCTTCTTGAGATCCTTTTTCGCGGCTAATCTGCTGCTGCAACAAAAACCCAC 5050
DB 3948 GATCTTCTTGAGATCCTTTTTCGCGGCTAATCTGCTGCTGCAACAAAAACCCAC 4007
QY 5051 CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTTACCACTCTTTTTCGGAAGTAA 5110
DB 4008 CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTTACCACTCTTTTTCGGAAGTAA 4067
QY 5111 CTGGCTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTGGCC 5170
DB 4068 CTGGCTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTGGCC 4127
QY 5171 ACCACTTCAGAACTCTGTAGCAGCGCTACATACCTCGCTGCTGCTAATCTGTTACAG 5230
DB 4128 ACCACTTCAGAACTCTGTAGCAGCGCTACATACCTCGCTGCTGCTAATCTGTTACAG 4187
QY 5231 TGCTGCTGCTGAGTGGGTAAGTCTGCTTACCGGTTGGAATCAAGACAGTAGTTAC 5290
DB 4188 TGCTGCTGCTGAGTGGGTAAGTCTGCTTACCGGTTGGAATCAAGACAGTAGTTAC 4247
QY 5291 CGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTGCTGCAACAGCCAGCTTGGAGC 5350
DB 4248 CGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTGCTGCAACAGCCAGCTTGGAGC 4307
QY 5351 GAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCCAGCTTC 5410
DB 4308 GAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCCAGCTTC 4367
QY 5411 CCGAAGCGAGAAAGCGCAGGTATCCGTAAGCGCAGGGTCCGAAACAGGAGAGCGCA 5470
DB 4368 CCGAAGCGAGAAAGCGCAGGTATCCGTAAGCGCAGGGTCCGAAACAGGAGAGCGCA 4427
QY 5471 CGAGGAGCTTCAGGGGGAACCGCTGATCTTTTATAGTCTGCTGCGGTTTCGCCACC 5530
DB 4428 CGAGGAGCTTCAGGGGGAACCGCTGATCTTTTATAGTCTGCTGCGGTTTCGCCACC 4487
QY 5531 TCTGACTTCAGCGTCCATTTTGTGATGCTGCTCAGGGGGGCGGCGCTATGGAAGACG 5590
DB 4488 TCTGACTTCAGCGTCCATTTTGTGATGCTGCTCAGGGGGGCGGCGCTATGGAAGACG 4547
QY 5591 CCAGCAACCGGGCTTTTACGGTCTCTGCGCTTTTGTGCGGCTTTTGTCTCATGTTCT 5650
DB 4548 CCAGCAACCGGGCTTTTACGGTCTCTGCGCTTTTGTGCGGCTTTTGTCTCATGTTCT 4607
QY 5651 TTCCTGCGTTATCCCTGATTCCTGGAATAACCGTATTAACCGCTTTGAGTGAAGCTGATA 5710
DB 4608 TTCCTGCGTTATCCCTGATTCCTGGAATAACCGTATTAACCGCTTTGAGTGAAGCTGATA 4667
QY 5711 CGCTCGCGCAGCCGAAACGACCGAGCGCAGCGAGTCACTGAGCAGGAGCGGAGAGC 5770

DB 4668 CCCTTCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGCTGAGCGTGGGTCTCGCG 4727
QY 5771 GCCCAATACGCAAAACCGCTCTCCCGCGGTTTGGCCGATTTCATTAAATGCAG 5822
DB 4728 GCCCAATACGCAAAACCGCTCTCCCGCGGTTTGGCCGATTTCATTAAATGCAG 4779

RESULT 7

US-09-991-209-33
; Sequence 33, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 5034
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJQ5 vector
US-09-991-209-33

Query Match 47.5%; Score 2768; DB 10; Length 5034;

Best Local Similarity 96.8%; Pred. No. 0;

Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCTCTTGGCGGTC 2894
DB 1889 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCTCTTGGCGGTC 1948
QY 2895 TTGCGATGATTATCATATATATTTCTGTTGAAATTTAGTTAAGCATGTAATAATTAAACATGT 2954
DB 1949 TTGCGATGATTATCATATATATTTCTGTTGAAATTTAGCATGTAATAATTAAACATGT 2008
QY 2955 AATGCAATGAGTTATTTATGAGATGGTTTTTATGATTAGATGCTCCGCAATTAACATTT 3014
DB 2009 AATGCAATGAGTTATTTATGAGATGGTTTTTATGATTAGATGCTCCGCAATTAACATTT 2068
QY 3015 AATACGCGATAGAAAACAAAATATAGCGCAAACTAGGATAAATTTATCCGCGCGGTGT 3074
DB 2069 AATACGCGATAGAAAACAAAATATAGCGCAAACTAGGATAAATTTATCCGCGCGGTGT 2128
QY 3075 CATCTATGTTACTAGATTCGACCTCGAGGATGGGATCCGCGGCGCATGCGACGTGGGC 3134
DB 2129 CATCTATGTTACTAGATTCGATAATACCTCTAGAGCGCGCGGTGGAGC-----T 2175
QY 3135 CCAATTCGCGCTTATAGTGAAGTGGTATTTAC---AATTCATTCGGCGCTGTTTAAACAGTC 3191
DB 2176 CCNATTCGCGCTTATAGTGAAGTGGTATTTACGCGGCTCAGTCGCGCTGTTTAAACAGTC 2235
QY 3192 GTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCCCTTTCGAGCAGCATCCCCCTTTCG 3251
DB 2236 GTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCCCTTTCGAGCAGCATCCCCCTTTCG 2295
QY 3252 CCAGCTGGCGTAAATAGCGAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTCGGGAGCC 3311
DB 2296 CCAGCTGGCGTAAATAGCGAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTCGGGAGCC 2355
QY 3312 TGAATGGCGCAAT--GGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGTGTGTTA 3370
DB 2356 TGAATGGCGCAATGGGAGCGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGTGTGTTA 2415


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Db 4521 TCTGACTTGAGCGTGGATTTTGTGATGCTTCGTGAGGGGGCGAGCGCTATGGAAGACG 4580
Qy 5591 CCAGCAACGCGGGCTTTTACGGTCTCTGGCCCTTTTGTGCTGGCCCTTTTGTCTCACATGTTCT 5650
Db 4581 CCAGCAACGCGGGCTTTTACGGTCTCTGGCCCTTTTGTGCTGGCCCTTTTGTCTCACATGTTCT 4640
Qy 5651 TTCTGCGTTATCCCTCGATCTCTGTGATTAACCGTATTACGGCTTTGAGTGAAGCTGATA 5710
Db 4641 TTCTGCGTTATCCCTCGATCTCTGTGATTAACCGTATTACGGCTTTGAGTGAAGCTGATA 4700
Qy 5711 CCGCTCGCCGAGCCGCAACGAGCGAGCGAGCGAGTCAGTGAAGCGAGCGAGCGAGCG 5770
Db 4701 CCGCTCGCCGAGCCGCAACGAGCGAGCGAGCGAGTCAGTGAAGCGAGCGAGCGAGCG 4760
Qy 5771 GCCCAATACGCAACCGCCCTCTCCCGCGCGTGTGGCCGATTCATTAATGCGAG 5822
Db 4761 GCCCAATACGCAACCGCCCTCTCCCGCGCGTGTGGCCGATTCATTAATGCGAG 4812

RESULT 8
US-09-991-209-36
; Sequence 36, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991.209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 5164
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pPQ10.1 vector
US-09-991-209-36

Query Match 47.5%; Score 2768; DB 10; Length 5164;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAACAACTTGGCAATAAGTTTCTTAAGATTGCAATCCCTGTCGCGTC 2894
Db 778 AAGCAGATCGTTCAACAACTTGGCAATAAGTTTCTTAAGATTGCAATCCCTGTTGCGCGTC 837
Qy 2895 TTGGGATGATTATCATATAATTTCTGTTGAATTACGTTTAAGCATGTAATAATTAACATGT 2954
Db 838 TTGGGATGATTATCATATAATTTCTGTTGAATTACGTTTAAGCATGTAATAATTAACATGT 897
Qy 2955 AATGCATGACGTTATTTATGAGATGGGTTTATGATTAGAGTCCCGCAATTAACATTT 3014
Db 898 AATGCATGACGTTATTTATGAGATGGGTTTATGATTAGAGTCCCGCAATTAACATTT 957
Qy 3015 AATACGGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATTAATGCGCGCGGTGT 3074
Db 958 AATACGGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATTAATGCGCGCGGTGT 1017
Qy 3075 CATCTATGTTACTAGATCGACCTCGAGCGATGGGATCCGCGCGCATGCGACGTGCGGC 3134
Db 1018 CATCTATGTTACTAGATCGATAGCTTCTAGAGCGCGCGGTGGAGC-----T 1064
Qy 3135 CCAATTGCGCCCTATAGTGAAGTGAATTAAC-----AATTCATGCGCGGTGTTTAAACAGTTC 3191
Db 1065 CCAATTGCGCCCTATAGTGAAGTGAATTAACCGCGCTCACTGCGCGTCTGTTTAAACAGTTC 1124
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Qy 3192 GTGACTGGGGAACCCCTGGCGTTACCCAACTTAATTCGCCCTTGAGGCAATCCCTCTTCG 3251
Db 1125 GTGACTGGGGAACCCCTGGCGTTACCCAACTTAATTCGCCCTTGAGGCAATCCCTCTTCG 1184
Qy 3252 CCAGCTGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC 3311
Db 1185 CCAGCTGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC 1244
Qy 3312 TGAATGCGCGAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTGTTA 3370
Db 1245 TGAATGCGCGAATGGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTGTTA 1304
Qy 3371 CGCGCAGCGTGACGCTACACTTGCAGCGCCCTAGCGCGCGCTCTTTCGCTTCTTC 3430
Db 1305 CGCGCAGCGTGACGCTACACTTGCAGCGCGCCCTAGCGCGCGCTCTTTCGCTTCTTC 1364
Qy 3431 CTTTCCTTTCGCGCACGTTTCGCGCGCTTTCGCGTCAAGCTCTAAATCGGGGGCTCCCTT 3490
Db 1365 CTTTCCTTTCGCGCACGTTTCGCGCGCTTTCGCGTCAAGCTCTAAATCGGGGGCTCCCTT 1424
Qy 3491 TAGGGTTCGATTTAGAGCTTTACGCACTCGACCGCAAAAAAATCTGATTTGGGTGATG 3550
Db 1425 TAGGGTTCGATTTAGTGTCTTACGGCACCTCGACCGCAAAAAAATCTGATTTAGGTGATG 1484
Qy 3551 GTTCACTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTGACGTTGAGTCCA 3610
Db 1485 GTTCACTAGTGGGCCATCGCCCTGATAGAGCGTTTTCGCCCTTTGACGTTGAGTCCA 1544
Qy 3611 CGTTCTTTAATAGTGAAGTCTTGTTCGCAACTGGGAAACACACTCAACCTATCTCGGTCT 3670
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Qy 3671 ATTCTTTGATTTAAGGATTTTTCGCGATTTTCGCGCTATTTGTTTAAAAAATGAGCTGA 3730
Db 1605 ATTCTTTGATTTAAGGATTTTTCGCGATTTTCGCGCTATTTGTTTAAAAAATGAGCTGA 1664
Qy 3731 TTTAAACAATATTTAAGCGCAATTTTAAACAATAATTAAGTTTACAAATTTTCGCTGATG 3790
Db 1665 TTTAAACAATATTTAAGCGCAATTTTAAACAATAATTAAGTTTACAAATTTTCGCTGATG 1715
Qy 3791 CGGTATTTCTCTCTTACGCACTGTGCGGTATTTTACACGCGCATACAGGTGGCACTTTTC 3850
Db 1716 -----AGTGGCACTTTTC 1729
Qy 3851 GGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATC 3910
Db 1730 GGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATC 1789
Qy 3911 CGCTCATGACACAATACCTGATAAATGCTTCAATAATTTGAAAGGAGGAGATGA 3970
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Qy 3971 GTATTCAACATTTTCGCTGCGCCCTTATTCCTTTTTTTCGCGCATTTTTCCTCTGTTT 4030
Db 1850 GTATTCAACATTTTCGCTGCGCCCTTATTCCTTTTTTTCGCGCATTTTTCCTCTGTTT 1909
Qy 4031 TTGCTCAACCCAGAAAACCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTCGACGAG 4090
Db 1910 TTGCTCAACCCAGAAAACCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTCGACGAG 1969
Qy 4091 TGGGTTACATCGAACTCGATCTCAACAGCGGTAGATCTTTGAGAGTTTTCGCCCGCAAG 4150
Db 1970 TGGGTTACATCGAACTCGATCTCAACAGCGGTAGATCTTTGAGAGTTTTCGCCCGCAAG 2029
Qy 4151 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTTGGCGCGGTATTTATCCCGTA 4210
Db 2030 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTTGGCGCGGTATTTATCCCGTA 2089
Qy 4211 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGATGCACTTGGTTG 4270
Db 2090 TTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGATGCACTTGGTTG 2149
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Qy	3015	AATACGGCGATAGAAAAACAAAATATAGCGCGCAAACTAGGATFAAATATATCGCGCGCGTGT	3074
Db	1074		
Qy	3075	CATCTATGTACTAGATGCACTTCGAGGCAATGGGATCGCGCGCGCATGCGAGTCTGGGC	3134
Db	1134	CATCTATGTTACTAGATCGATAAGCTTCTTAGAGCGCGCGTGGAGC-----T	1180
Qy	3135	CCAAATTCGCCCTATAGTGAGTCGTATTAC--AAATTCACATGGCGCGTGGTATTAACAAGTC	3191
Db	1181		
Qy	3192	GTGACTGGGAAAAACCTCTGGCGTTACCCAACTTAATCGCTTTCGACGACATATCCCTCTTCG	3251
Db	1241	GTGACTGGGAAAAACCTCTGGCGTTACCCAACTTAATCGCTTTCGACGACATATCCCTCTTCG	1300
Qy	3252	CCAGCTCGCGTAAATAGCGAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCC	3311
Db	1301	CCAGCTCGCGTAAATAGCGAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCC	1360
Qy	3312	TGAATGCGCAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGGTGGTGGTTA	3370
Db	1361		
Qy	3371	CGCGACGCGTGACCGCTACACTTCCGACGCGCCCTAGCGCCCGCTCTCTTTCGCTTCTTCTCC	3430
Db	1421	CGCGACGCGTGACCGCTACACTTCCGACGCGCCCTAGCGCCCGCTCTCTTTCGCTTCTTCTCC	1480
Qy	3431	CTTCTCTTTCGCGCACGTTTCGCGCTTTCGCCGTGAAGCTCTAAATCGGGGGGTCTCCCTT	3490
Db	1481	CTTCTCTTTCGCGCACGTTTCGCGCTTTCGCCGTGAAGCTCTAAATCGGGGGGTCTCCCTT	1540
Qy	3491	TAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGSGTGAAG	3550
Db	1541		
Qy	3551	GTTCACTAGTGGGCGCATCGCCCTGTATAGACGGTTTTTCGCCCTTTGACCTTCGAGTCCA	3610
Db	1601	GTTCACTAGTGGGCGCATCGCCCTGTATAGACGGTTTTTCGCCCTTTGACCTTCGAGTCCA	1660
Qy	3611	CGTTCTTTAATAGTGGACTCTGTGTTCAAACTGTGAACAACACTCAACCCCTATCTCGGTCT	3670
Db	1661	CGTTCTTTAATAGTGGACTCTGTGTTCAAACTGTGAACAACACTCAACCCCTATCTCGGTCT	1720
Qy	3671	ATTCCTTTGATTTATAGGGAATTTGCGCATTTTCGCCCTATGCGTCTTAAAAAATGAGCTGA	3730
Db	1721	ATTCCTTTGATTTATAGGGAATTTGCGCATTTTCGCCCTATGCGTCTTAAAAAATGAGCTGA	1780
Qy	3731	TTTAAACAAATATTTAAGCGAAATTTTAAACAAATATTTAAGCTTTTACAAATTCGCCCTGATG	3790
Db	1781	TTTAAACAAATATTTAAGCGAAATTTTAAACAAATATTTAAGCTTTTACAAATTCGCCCTGATG	1831
Qy	3791	CGGTATTTTCTCTTACCGCATCTGTGCGGTATTTTCACACCGGCATACAGTGGCACTTTTTC	3850
Db	1832	-----AGGTGGCACTTTTTC	1845
Qy	3851	GGGGAAATGTGCGGGAAACCCCTATTTGTTTATTTTCTAAATACATCTCAAAATATGTATC	3910
Db	1846	GGGGAAATGTGCGGGAAACCCCTATTTGTTTATTTTCTAAATACATCTCAAAATATGTATC	1905
Qy	3911	CGCTCATGAGACAAATAACCCCTGATAAATGCTTCAATAATATCGAAAGGAAGAGTATGA	3970
Db	1906	CGCTCATGAGACAAATAACCCCTGATAAATGCTTCAATAATATCGAAAGGAAGAGTATGA	1965
Qy	3971	GTATTCACAAATTTCCGTGTGCGCCCTTATCCCTTTTTCGGGCAATTTTGCTTCTCTGTTT	4030
Db	1966	GTATTCACAAATTTCCGTGTGCGCCCTTATCCCTTTTTCGGGCAATTTTGCTTCTCTGTTT	2025
Qy	4031	TTGCTCACCCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG	4090
Db	2026	TTGCTCACCCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG	2085

Qy	4091	TGGTTCATCGAACTCGGATCTCAACAGCGGGTAAGATCTCTTGAGAGTGTTCGCGCCCGAAG	4155
Db	2086	TGGGTTACATCGAACTGGATCTCAACAGCGGGTAAGATCTCTTGAGAGTGTTCGCGCCCGAAG	2145
Qy	4151	AAAGTTTTCCAAATGATGAGCACATTTTAAAGTTCCTGCTATCTGTCGCGGGTATTTATCCCGTA	4210
Db	2146	AAAGTTTTCCAAATGATGAGCACATTTTAAAGTTCCTGCTATCTGTCGCGGGTATTTATCCCGTA	2205
Qy	4211	TTGACGCGGGCAAGAGCAACTCGGTCGCGGCATACACTATTCTCAGAAATGACTTCGGTTG	4270
Db	2206	TTGACGCGGGCAAGAGCAACTCGGTCGCGGCATACACTATTCTCAGAAATGACTTCGGTTG	2265
Qy	4271	AGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTAATGCA	4330
Db	2266	AGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTAATGCA	2325
Qy	4331	GTGCTGCGCAATACCATGATGATGATAACACTGGCGCCAACTTACTTCTGACAAAGCATCGGAG	4390
Db	2326	GTGCTGCGCAATACCATGATGATGATAACACTGGCGCCAACTTACTTCTGACAAAGCATCGGAG	2385
Qy	4391	GACCGAAGGAGCTAAACCGCTTTTTTTGCAAAATGCGGGATCATGTAACTCGCCTTTGATC	4450
Db	2386	GACCGAAGGAGCTAAACCGCTTTTTTTGCAAAATGCGGGATCATGTAACTCGCCTTTGATC	2445
Qy	4451	GTGCGGAAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACACAGATGCCTG	4510
Db	2446	GTGCGGAAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACACAGATGCCTG	2505
Qy	4511	TAGCAATGGCAACAAAGTTGCGCAAACTATTAACTGGCGAACTTACTTCTAGCTTTCCC	4570
Db	2506	TAGCAATGGCAACAAAGTTGCGCAAACTATTAACTGGCGAACTTACTTCTAGCTTTCCC	2565
Qy	4571	GGCAACAAATTAATAGACTGGAATGGAGCGGATAAAAGTTGCAGGACCACTTCTCGCTCGG	4630
Db	2566	GGCAACAAATTAATAGACTGGAATGGAGCGGATAAAAGTTGCAGGACCACTTCTCGCTCGG	2625
Qy	4631	CCCTTCGCGCTGCGTTTATTTCTGATAAATCTCGAGCCGGTGAGCGTGGGTCTCGCG	4690
Db	2626	CCCTTCGCGCTGCGTTTATTTCTGATAAATCTCGAGCCGGTGAGCGTGGGTCTCGCG	2685
Qy	4691	GTATCATTTGACGACCTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA	4750
Db	2686	GTATCATTTGACGACCTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGA	2745
Qy	4751	CGGGAGTCAAGGCAACTATGGATGAAACGAAATAGACAGATCGCTGAGATAGGTGCCTCAC	4810
Db	2746	CGGGAGTCAAGGCAACTATGGATGAAACGAAATAGACAGATCGCTGAGATAGGTGCCTCAC	2805
Qy	4811	TGATTAAGCAATCGGTAACTGTGTGACAAAGTTTACTCATATATATCTTTAGATTGATTTAA	4870
Db	2806	TGATTAAGCAATCGGTAACTGTGTGACAAAGTTTACTCATATATATCTTTAGATTGATTTAA	2865
Qy	4871	AACTTCATTTTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGTATATCTCATGACCA	4930
Db	2866	AACTTCATTTTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGTATATCTCATGACCA	2925
Qy	4931	AAATCCCTTAAACGTGAGTTTTTCGTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAAAG	4990
Db	2926	AAATCCCTTAAACGTGAGTTTTTCGTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAAAG	2985
Qy	4991	GATCTTCTTGAGATCCCTTTTTTTCTCGGGGTAACTGTGCTTGTGCAAAACAAAAAACCCAC	5050
Db	2986	GATCTTCTTGAGATCCCTTTTTTTCTCGGGGTAACTGTGCTTGTGCAAAACAAAAAACCCAC	3045
Qy	5051	CGCTACCGGGTGTGTGTTTTCGCGGATCAAGAGCTACCACTCTTTTTCGAGAGTTAA	5110
Db	3046	CGCTACCGGGTGTGTGTTTTCGCGGATCAAGAGCTACCACTCTTTTTCGAGAGTTAA	3105
Qy	5111	CTGGCTTCAGCAGCGGCAGATACCAAATACTGCTCTTCTAGTGTAGCCGTAGTTAGGCC	5170
Db	3106	CTGGCTTCAGCAGCGGCAGATACCAAATACTGCTCTTCTAGTGTAGCCGTAGTTAGGCC	3165
Qy	5171	ACCACTTCAAGAACTCTGTAGACACCGCTACATACCTCGCTCTGTCTATCTCGTTACCAAG	5230

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Qy 5351 GAAACGACCTACACCGAACTGAGATACCTACAGCTGAGCTATGAGAAAGCGCCAGCTTC 5410
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Qy 5651 TTCCTGCTTATCCCTGATCTGTGGATAACCGTATTTACCGCTTTTACGAGCTGATA 5710
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Qy 5711 CGGCTCGCGGAGCGAAGCGAGCGAGCGAGCTAGTACGAGCGAAGCGGAGAGC 5770
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RESULT 10

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; Sequence 38, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pUG4 vector
US-09-991-209-38
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Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
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Qy |||||
5651 TTCTGCTGTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTCTGAGTGAAGTATA 5710
Db |||||
3664 TTCTGCTGTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTCTGAGTGAAGTATA 3723
Qy |||||
5711 CCGCTGCGCGCAGCGCAACCGAGCGCAGCGAGTCAAGTCAAGCGAGGAGGAGGAGGAGG 5770
Db |||||
3724 CCGCTGCGCGCAGCGCAACCGAGCGCAGCGAGTCAAGTCAAGCGAGGAGGAGGAGGAGG 3783
Qy |||||
5771 GCCCAATACGCAACCGCTCTTCCCGCGGTTGGCGGATTCATTAATGCAAG 5822
Db |||||
3784 GCCCAATACGCAACCGCTCTTCCCGCGGTTGGCGGATTCATTAATGCAAG 3835

RESULT 11

US-09-991-209-27
; Sequence 27, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP4a2 vector
US-09-991-209-27

Query Match          47.5%; Score 2768; DB 10; Length 5327;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATTGAATCTGTCGGGTC 2894
Db 720 AAGCAGATCGTTCAACATTTGGCAATAAAGTTTCTTAAGATTGAATCTGTCGGGTC 779

Qy 2895 TTGGATGATTAATCATATAATTTCTGTGAATAGTTAAGCATGTAATAATTAACATGT 2954
Db 780 TTGGATGATTAATCATATAATTTCTGTGAATAGTTAAGCATGTAATAATTAACATGT 839

Qy 2955 AATCATGACGTTAATTTATGATGAGTGGTTTATGATTTAGAGTCCCGCAATTTATACATTT 3014
Db 840 AATCATGACGTTAATTTATGATGAGTGGTTTATGATTTAGAGTCCCGCAATTTATACATTT 899

Qy 3015 AATACGGATAGAAAAACAAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGT 3074
Db 900 AATACGGATAGAAAAACAAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGT 959

Qy 3075 CATCTATGTTACTAGATCGACCTCGAGGATGGGATCGCGCGCGCATGGACGTGGGC 3134
Db 960 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGGAGC-----T 1006

Qy 3135 CCAATTCGCGCTATAGTAGTGTGTAATAC---AATTCACTGGCGCTGTTTACACGTC 3191
Db 1007 CCAATTCGCGCTATAGTAGTGTGTAATACGGCGCTCATGCGCGTGTGTTTACACGTC 1066

Qy 3192 GTGACTGGGAAAAACCTCGGCTTACCCAACTTAATCGCCTTTCAGCACATCCCGCTTTTCG 3251
Db 1067 GTGACTGGGAAAAACCTCGGCTTACCCAACTTAATCGCCTTTCAGCACATCCCGCTTTTCG 1126

Qy 3252 CCAGCTGGGTAATAGGAGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC 3311
Db 1127 CCAGCTGGGTAATAGGAGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCGAGCC 1186

Qy 3312 TGAATGCGGAAT--GGAAGCGCCCTGAGCGCGCATTAAGCGCGCGGTGTTGTTGTTA 3370
Db 1187 TGAATGCGGAATGGAAGCGCCCTGAGCGCGCATTAAGCGCGCGGTGTTGTTGTTA 1246

Qy 3371 CGCGCAGCGTGACCGCTACACTTCCAGCGCCCTTAGCGCCCGCTCTTTCGCTTTCTTTC 3430
Db 1247 CGCGCAGCGTGACCGCTACACTTCCAGCGCCCTTAGCGCCCGCTCTTTCGCTTTCTTTC 1306

Qy 3431 CTTTCCTTTCTCGCCACGCTTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGGGGCTCCCTT 3490
Db 1307 CTTTCCTTTCTCGCCACGCTTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGGGGCTCCCTT 1366

Qy 3491 TAGGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAACTTGAATTTGGGTGATG 3550
Db 1367 TAGGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAACTTGAATTTAGGGTGA 1426

Qy 3551 GTTCACGTAGTGGCCATCGCCCTGTAGAGCGGTTTTTCGCGCTTTGACCGTTGGAGTCCA 3610
Db 1427 GTTCACGTAGTGGCCATCGCCCTGTAGAGCGGTTTTTCGCGCTTTGACCGTTGGAGTCCA 1486

Qy 3611 CGTTCTTTAATAGTGAATCTTTGTTCCAACTCGAACTCGAACTCAACCTTATCTCGGTCT 3670
Db 1487 CGTTCTTTAATAGTGAATCTTTGTTCCAACTCGAACTCGAACTCAACCTTATCTCGGTCT 1546

Qy 3671 ATTCTTTTGAATTAAGGATTTTCGGATTTTCGGCTATTTGGTTAAAAAATGAGCTGA 3730
Db 1547 ATTCTTTTGAATTAAGGATTTTCGGATTTTCGGCTATTTGGTTAAAAAATGAGCTGA 1606

Qy 3731 TTTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTTACAAATTTCCGCTGATG 3790
Db 1607 TTTAAACAAATATTTAAACGCGAATTTTAAACAAATATTTAAACGTTTACAAATTT----- 1657

Qy 3791 CGGTATTTTCTCTCTTACGCACTCTGCGGTATTTACACACCGCATACAGTGCACCTTTTC 3850
Db 1658 -----AGGTGCACTTTTC 1671

Qy 3851 GGGGAAATGTGCGGGAACCCCTAATTTTGTATTTTCTTAATACATTTCAATATGTATTC 3910
Db 1672 GGGGAAATGTGCGGGAACCCCTAATTTTGTATTTTCTTAATACATTTCAATATGTATTC 1731

Qy 3911 CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATAATGAAAAAGGAAGATGTA 3970
Db 1732 CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATAATGAAAAAGGAAGATGTA 1791

Qy 3971 GTATTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGCGCATTTTTCGCTTTCTGTTT 4030
Db 1792 GTATTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGCGCATTTTTCGCTTTCTGTTT 1851

Qy 4031 TTGCTCAACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 4090
Db 1852 TTGCTCAACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGAG 1911

Qy 4091 TGGGTTATCATGCAACTGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCCGAG 4150
Db 1912 TGGGTTATCATGCAACTGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCCGAG 1971

Qy 4151 AACGTTTTCGAATCATGAGCACTTTTAAAGTTCTGCTATGTTGGCGGTATTTATCCCGTA 4210
Db 1972 AACGTTTTCGAATCATGAGCACTTTTAAAGTTCTGCTATGTTGGCGGTATTTATCCCGTA 2031

Qy 4211 TTGAGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTTCTCAGAAATGACTTGGTTG 4270
Db 2032 TTGAGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTTCTCAGAAATGACTTGGTTG 2091

Qy 4271 AGTACTCAGCATGACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATATGCA 4330
Db 2092 AGTACTCAGCATGACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATATGCA 2151

Qy 4331 GTGCTGCATTAACCATGAGTGAATAACTGCGGCAACTTACTTCTGACAAAGATCGGAG 4390
Db 2152 GTGCTGCATTAACCATGAGTGAATAACTGCGGCAACTTACTTCTGACAAAGATCGGAG 2211

Qy 4391 GACCGAAGGAGCTAAACCGCTTTTTCACAAACATGCGGAGATCATGTAACTCGCTTGATC 4450
Db 2212 GACCGAAGGAGCTAAACCGCTTTTTCACAAACATGCGGAGATCATGTAACTCGCTTGATC 2271

Qy 4451 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAAACGAGCGGTGACACAGATGCGCTG 4510
Db 2272 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAAACGAGCGGTGACACAGATGCGCTG 2331

Qy 4511 TAGCAATGGCAACCAACCTGCGCAACTTATTAACCTGGCAACTTACTTCTAGCTTCCC 4570
Db 2332 TAGCAATGGCAACCAACCTGCGCAACTTATTAACCTGGCAACTTACTTCTAGCTTCCC 2391

Qy 4571 GGCACAAATTAATAGATGGAATGAGGCGGATTAAGTTGCAAGGACCACTTCTGCGCTCGG 4630
Db 2392 GGCACAAATTAATAGATGGAATGAGGCGGATTAAGTTGCAAGGACCACTTCTGCGCTCGG 2451

Qy 4631 CCCTTCGCGCTGGCTGTTTATTCCTGATTAATCTCGAGCCGTTGAGCGGTGCGGTCTCGG 4690
Db 2452 CCCTTCGCGCTGGCTGTTTATTCCTGATTAATCTCGAGCCGTTGAGCGGTGCGGTCTCGG 2511

Qy 4691 GTATCATTTGAGCACTGCGGCGCATGTAAGCCCTCCGCTATCTAGTTATCTACACGA 4750
Db 2512 GTATCATTTGAGCACTGCGGCGCATGTAAGCCCTCCGCTATCTAGTTATCTACACGA 2571

Qy 4751 CGGGAGTTCAGGCAACTTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTCAC 4810
Db 2572 CGGGAGTTCAGGCAACTTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTCAC 2631

Qy 4811 TGATTAAGCATTTGGTAACTGTTCAGACCAAGTTTACTCATATATATCTTTAGATTGATTAA 4870
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[illegible]

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1  APPLICANT: Dunn-Coleman, Nigel
2  APPLICANT: Langdon, Timothy
3  APPLICANT: Morse, Phillip
4  TITLE OF INVENTION: Manipulation of the Phenolic Acid
5  TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
6  TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
7  FILE REFERENCE: GC648-2
8  CURRENT APPLICATION NUMBER: US/09/991,209
9  CURRENT FILING DATE: 2002-07-02
10 PRIOR APPLICATION NUMBER: US 60/249,608
11 PRIOR FILING DATE: 2000-11-17
12 NUMBER OF SEQ ID NOS: 97
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 19
15 LENGTH: 5337
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: pTU4 vector
20 US-09-991-209-19

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Query Match	47.5%;	Score 2768;	DB 10;	Length 5337;
Best Local Similarity	96.8%;	Pred. No. 0;		
Matches 2895;	Conservative 0;	Mismatches 25;	Indels 72;	Gaps 4;
Qy	2835	AAGCAGATCGTTCAAACATTTGGCAATRAAGTTTCTTAAGATTGAATCCGTGTGCGGTC	2894	
Db	954	AAGCAGATCGTTCAAACATTTGGCAATRAAGTTTCTTAAGATTGAATCCGTGTGCGGTC	1013	
Qy	2895	TTCCGATGATTATCATATAATTTTCGTTGAAATAGCTTAAGCATGTATAATAAATACATGT	2954	
Db	1014	TTCCGATGATTATCATATAATTTTCGTTGAAATAGCTTAAGCATGTATAATAAATACATGT	1073	
Qy	2955	AATGCAATGAGTTATTTATGAGATGGGTTTTATGATTTAGAGTCCGCAATTTATCATTTT	3014	
Db	1074	AATGCAATGAGTTATTTATGAGATGGGTTTTATGATTTAGAGTCCGCAATTTATCATTTT	1133	
Qy	3015	AATACGCGATAGAAACAAAATATAGCGCGCAAACTAGGATAAAATTTATCGCGCGGGTGT	3074	
Db	1134	AATACGCGATAGAAACAAAATATAGCGCGCAAACTAGGATAAAATTTATCGCGCGGGTGT	1193	
Qy	3075	CATCTATGTTACTAGATCGACCTGCAGGCGATGGGATCGCGCGCGCATGCGACGTGGGC	3134	
Db	1194	CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGTGGAGC-----T	1240	
Qy	3135	CGAATTCGCGCTATAGTAGAGTCGTATTAAC-----AATTCATCGCGCGTGGTTTTACAAAGTC	3191	
Db	1241	CGAATTCGCGCTATAGTAGAGTCGTATTAACCGCGCTCACTGCGCGCTCGTTTTACAAAGTC	1300	
Qy	3192	GTGACCTGGCAAAACCTGCGGTTTACCACATTAATAGCCTTGACACACATCCCCCTTTGCG	3251	
Db	1301	GTGACCTGGCAAAACCTGCGGTTTACCACATTAATAGCCTTGACACACATCCCCCTTTGCG	1360	
Qy	3252	CCAGCTGGCGTAAATACGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC	3311	
Db	1361	CCAGCTGGCGTAAATACGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC	1420	
Qy	3312	TGAATGGCGAAT--GGAACGCGCCTGTAGCGGCGCAATTAAGCGCGCGGGTGTGGTTA	3370	
Db	1421	TGAATGGCGAATGGGAACGCGCCCTGTAGCGGCGCATTAAGCGCGCGGGTGTGGTTA	1480	
Qy	3371	CGCGGAGCTGACCGGTACACTTGGCAGGCGCCTAGCGCGCTCCTTTGCTTCTCTCC	3430	
Db	1481	CGCGGAGCTGACCGGTACACTTGGCAGGCGCCTAGCGCGCTCCTTTGCTTCTCTCC	1540	
Qy	3431	CTTCTCTTCTCGCCACGTTTCGCGGCTTTCGCCGTCAAGCTCTAAATCGGGGCTCCCTT	3490	
Db	1541	CTTCTCTTCTCGCCACGTTTCGCGGCTTTCGCCGTCAAGCTCTAAATCGGGGCTCCCTT	1600	
Qy	3491	TAGGGTTCCGATTTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATG	3550	
Db	1601	TAGGGTTCCGATTTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATG	1660	

Qy	3551	GTTCACCTAGTGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGGTTGGAGTCCA	3610		Db	2686	CCCTTCGGCTGGCTGGTTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGCTCTCGCG	2745	
Db	1661		1720		Qy	4691	GTATCATTTGACGACTCGGGCCAGATGGTAAGCCCTCCCGCTATCGTAGTATCTACACGA	4750	
Qy	3611	CGTTCTTTAATAGTGGACTCTGTTGTCABAACTGGAACAACTCAACCCCTATCTGGGTCT	3670		Db	2746	GTATCATTTGACGACTCGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTATCTACACGA	2805	
Db	1721	CGTTCTTTAATAGTGGACTCTGTTGTCABAACTGGAACAACTCAACCCCTATCTGGGTCT	1780		Qy	4751	CGGGAGCTCAGGCAACTATATGATGAAACGAATAGACAGATCGCTGAGATAGGTGCTCAC	4810	
Qy	3671	ATTCTTTTGATTTATAAGGGAATTTTGGCGATTTTCGGCTATTTGGTTAAATAATGAGCTGA	3730		Db	2806	CGGGAGCTCAGGCAACTATGATGAAACGAATAGACAGATCGCTGAGATAGGTGCTCAC	2865	
Db	1781	ATTCTTTTGATTTATAAGGGAATTTTGGCGATTTTCGGCTATTTGGTTAAATAATGAGCTGA	1840		Qy	4811	TGATTAAGCATTTGTTAACTGTCTGACAGCAAGTTTACTCATATATCTTTAGATGATTTAA	4870	
Qy	3731	TTTAAACAAATATTAAAGCAATTTTAAACAAATATTAAAGTTTAAATAATGAGCTGATG	3790		Db	2866	TGATTAAGCATTTGTTAACTGTCTGACAGCAAGTTTACTCATATATCTTTAGATGATTTAA	2925	
Db	1841	TTTAAACAAATATTAAAGCAATTTTAAACAAATATTAAAGTTTAAATAATGAGCTGATG	1891		Qy	4871	AATCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTGATATCTCATGACCA	4930	
Qy	3791	CGGTATTTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGGTGGCACTTTTC	3850		Db	2926	AATCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTGATATCTCATGACCA	2985	
Db	1892	-----AGGTGGCACTTTTC-----	1905		Qy	4931	AAATCCCTTAAAGTGGTTTTTCCTTCACTGAGCGTCAAGCCCGTAGAAGATCAAG	4990	
Qy	3851	GGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAATATGTATC	3910		Db	2986	AAATCCCTTAAAGTGGTTTTTCCTTCACTGAGCGTCAAGCCCGTAGAAGATCAAG	3045	
Db	1906	GGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAATATGTATC	1965		Qy	4991	GATCTTCTTGAGATCTTTTCTGCGCGTAATCTGCTGCTTGCARACAAACCAACAC	5050	
Qy	3911	CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATATTGAAAGGAAGATATGA	3970		Db	3046	GATCTTCTTGAGATCTTTTCTGCGCGTAATCTGCTGCTTGCARACAAACCAACAC	3105	
Db	1966	CGCTCATGAGACAATAACCCCTGATAAATGCTTCAATATATTGAAAGGAAGATATGA	2025		Qy	5051	CGCTACACGCGTGTGTTGTTGCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAA	5110	
Qy	3971	GTATTCACATTTCCGTTGTCGCCCTATTTCCCTTTTGTGGCGCATTTTGCCTTCTGTTT	4030		Db	3106	CGCTACACGCGTGTGTTGTTGCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAA	3165	
Db	2026	GTATTCACATTTCCGTTGTCGCCCTATTTCCCTTTTGTGGCGCATTTTGCCTTCTGTTT	2085		Qy	5111	CTGCTTTCAGCAGCGCGAGATACCAATATCTGCTCTTCTAGTGTAGCGGTAGTGGCC	5170	
Qy	4031	TTGCTCACCCAGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGTTGGGTGCACGAG	4090		Db	3166	CTGCTTTCAGCAGCGCGAGATACCAATATCTGCTCTTCTAGTGTAGCGGTAGTGGCC	3225	
Db	2086	TTGCTCACCCAGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGTTGGGTGCACGAG	2145		Qy	5171	ACCACTTCAAGAACTCTGTGACACCGCTACATACCTCGCTCTGCTATCTGTTTACCAG	5230	
Qy	4091	TGGGTATCATGAACTGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAAG	4150		Db	3226	ACCACTTCAAGAACTCTGTGACACCGCTACATACCTCGCTCTGCTATCTGTTTACCAG	3285	
Db	2146	TGGGTATCATGAACTGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAAG	2205		Qy	5231	TGGCTGTCTCCAGTGGCGGATAAGTCTGTCTTTACCGGTTTGGACTCAAGAGCATAGTTAC	5290	
Qy	4151	AACGTTTTCGAATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGTA	4210		Db	3286	TGGCTGTCTCCAGTGGCGGATAAGTCTGTCTTTACCGGTTTGGACTCAAGAGCATAGTTAC	3345	
Db	2206	AACGTTTTCGAATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGTA	2265		Qy	5291	CGGATAAGCGCGACGCGTCTGGGTGAAACGGGGGTTCTGTGACACAGCCGCTTGGAGC	5350	
Qy	4211	TTGACGCGCGCAAGAGCAACTCGTGCAGCATACACTATTTCTCAGAACTGCTTGGTTG	4270		Db	3346	CGGATAAGCGCGACGCGTCTGGGTGAAACGGGGGTTCTGTGACACAGCCGCTTGGAGC	3405	
Db	2266	TTGACGCGCGCAAGAGCAACTCGTGCAGCATACACTATTTCTCAGAACTGCTTGGTTG	2325		Qy	5351	GAAACGCTACACCGAACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCACGCTTC	5410	
Qy	4271	AGTACTCACAGTCAAGAAAGCATTTTACGGATGGCATGACAGTAAAGAAATTTATGCA	4330		Db	3406	GAAACGCTACACCGAACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCACGCTTC	3465	
Db	2326	AGTACTCACAGTCAAGAAAGCATTTTACGGATGGCATGACAGTAAAGAAATTTATGCA	2385		Qy	5411	CCGAAGGAGAAAGCGGACAGGTATCCGGTAAGCGCGGAGGTTCGAAACAGGAGAGCGCA	5470	
Qy	4331	GTGCTGCCATTAACATGATGATTAACATGCGGCCCACTTACTTCTGACACGATCGGAG	4390		Db	3466	CCGAAGGAGAAAGCGGACAGGTATCCGGTAAGCGCGGAGGTTCGAAACAGGAGAGCGCA	3525	
Db	2386	GTGCTGCCATTAACATGATGATTAACATGCGGCCCACTTACTTCTGACACGATCGGAG	2445		Qy	5471	CGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTTATAGTCTCTGCGGTTTCCGACCC	5530	
Qy	4391	GACCGAAGGAGCTAACCCCTTTTGTGACAACTGGGGGATCATGTAACTCGCCTTGATC	4450		Db	3526	CGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTTATAGTCTCTGCGGTTTCCGACCC	3585	
Db	2446	GACCGAAGGAGCTAACCCCTTTTGTGACAACTGGGGGATCATGTAACTCGCCTTGATC	2505		Qy	5531	TCTGACTTGAAGCTCGATTTTGTGATGCTGCTGAGGGGGGGGAGCTTATGGAAGAAACG	5590	
Qy	4451	GTGCGGAAACCGGAGCTGAATGAAGCCATACAAACGACGAGGTGACACCGATGCGCTG	4510		Db	3586	TCTGACTTGAAGCTCGATTTTGTGATGCTGCTGAGGGGGGGGAGCTTATGGAAGAAACG	3645	
Db	2506	GTGCGGAAACCGGAGCTGAATGAAGCCATACAAACGACGAGGTGACACCGATGCGCTG	2565		Qy	5591	CCAGCAACCGCGCTTTTAAAGGCTTCTGCGCTTTTGTGCGCTTTTGTCTCATGTTCT	5650	
Qy	4511	TAGCAATGCCAACACGTTGGCAACTATTAACTGGCGCACTTACTTACTTACTGCTTCCC	4570		Db	3646	CCAGCAACCGCGCTTTTAAAGGCTTCTGCGCTTTTGTGCGCTTTTGTCTCATGTTCT	3705	
Db	2566	TAGCAATGCCAACACGTTGGCAACTATTAACTGGCGCACTTACTTACTTACTGCTTCCC	2625		Qy	5651	TTCTGCTTATTCCTCAATCTGTGGAATAACCGTATTTACCGCTTTTGTGAGTGTGATTA	5710	
Qy	4571	GCCAAACAATTAATGACTGGAATGAGGCGGATTAAGTTTGCAGGACCACTTCTGCGCTCGG	4630		Db	3706	TTCTGCTTATTCCTCAATCTGTGGAATAACCGTATTTACCGCTTTTGTGAGTGTGATTA	3765	
Db	2626	GCCAAACAATTAATGACTGGAATGAGGCGGATTAAGTTTGCAGGACCACTTCTGCGCTCGG	2685		Qy	5711	CCGCTCGCGCGCAGCGCAACCGAGCCGAGCTCAGTGTAGCGGAGCGGAGAGCAGC	5770	
Qy	4631	CCCTTCGCGCTGGCTGTTTTATTGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCG	4690						

Db 3766 CCCTCGCCGACGCGGAAACGACGAGCGAGCGAGTCAGTGAAGCGAGGAAGAGC 3825
Qy 5771 GCCAATACGCAACCGCTCTCCCGCGGTTGGCCGATTCATTAATGCAG 5822
Db 3826 GCCAATACGCAACCGCTCTCCCGCGGTTGGCCGATTCATTAATGCAG 3877

RESULT 13
US-09-991-209-23
; Sequence 23, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 5337
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP8-5 vector
US-09-991-209-23

Query Match 47.5%; Score 2768; DB 10; Length 5337;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATTCCTGTTGCCGGTC 2894
Db 954 AAGCAGATCGTTCCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATTCCTGTTGCCGGTC 1013

Qy 2895 TTGGGATGATTATCATATTAATTTCTGTGAATTAAGTGAAGCATGTAATTAATTAACATGT 2954
Db 1014 TTGGGATGATTATCATATTAATTTCTGTGAATTAAGTGAAGCATGTAATTAATTAACATGT 1073

Qy 2955 AATGCATGATGTTATTTATGAGATGGTGTATGATTAAGTTCGCGCAATTAATTAATTAAT 3014
Db 1074 AATGCATGATGTTATTTATGAGATGGTGTATGATTAAGTTCGCGCAATTAATTAATTAAT 1133

Qy 3015 AATACGCGATAGAAAACAAATAATAGCGGCAAACTAGGATAAATTAATCGCGCGGTGT 3074
Db 1134 AATACGCGATAGAAAACAAATAATAGCGGCAAACTAGGATAAATTAATCGCGCGGTGT 1193

Qy 3075 CATCTATGTTACTAGATCGACCTGCGAGCATGGATTCGCGGCGCATGCGAGCTCGGC 3134
Db 1194 CATCTATGTTACTAGATCGATTAAGTTCCTAGACGCGCGGTGGAGC-----T 1240

Qy 3135 CCAATTCGCGCTATAGTGTGCTATTAC---AATTCATGCGCGCTGTTTACAAACGTC 3191
Db 1241 CCAATTCGCGCTATAGTGTGCTATTACGCGCGCTCATGCGCGCTGTTTACAAACGTC 1300

Qy 3192 GTGACTGGGAAAACCTGGCGTTACCAACTTAATCGCTTTCGAGCAATPCCCTTTTCG 3251
Db 1301 GTGACTGGGAAAACCTGGCGTTACCAACTTAATCGCTTTCGAGCAATPCCCTTTTCG 1360

Qy 3252 CCAGCTGGGTAATAGGAGAGCGCGCATGCGCTTCCACAGTTGCGGAGCC 3311
Db 1361 CCAGCTGGGTAATAGGAGAGCGCGCATGCGCTTCCACAGTTGCGGAGCC 1420

Qy 3312 TGAATGCGCAAT--GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGCTGTGA 3370
Db 1421 TGAATGCGCAATGCGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGCTGTGA 1480

Qy 3371 CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCCGCTCTCTTTCGCTTCTTCC 3430
Db 1481 CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCCGCTCTCTTTCGCTTCTTCC 1540

Qy 3431 CTTTCCTTTCTCGCCACGTTTCGCCGGCTTCCCGCTCAAGCTCTAATAATCGGGGCTCCCTT 3490
Db 1541 CTTTCCTTTCTCGCCACGTTTCGCCGGCTTCCCGCTCAAGCTCTAATAATCGGGGCTCCCTT 1600

Qy 3491 TAGGGTTCGGAATTTAGAGCTTTTACGCACTTCGACCGCAAAAAAATTTGATTTGGGTGATG 3550
Db 1601 TAGGGTTCGGAATTTAGAGCTTTTACGCACTTCGACCGCAAAAAAATTTGATTTAGGGTGA 1660

Qy 3551 GTTCAGTAGTGGGCCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGAGTCCA 3610
Db 1661 GTTCAGTAGTGGGCCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGAGTCCA 1720

Qy 3611 CGTTCTTTAATAGTGCACCTCTGTTCCAACTCGAACTCAACACTCAACCTCTATCTCGGTCT 3670
Db 1721 CGTTCTTTAATAGTGCACCTCTGTTCCAACTCGAACTCAACACTCAACCTCTATCTCGGTCT 1780

Qy 3671 ATTCTTTTGAATTTAAGGGAATTTTGCAGATTTTGCCTATTGCTTAAAAAATAGAGCTGA 3730
Db 1781 ATTCTTTTGAATTTAAGGGAATTTTGCAGATTTTGCCTATTGCTTAAAAAATAGAGCTGA 1840

Qy 3731 TTAAACAATATTTAAACGGGAATTTTAAACAATATTAAGCTTTTACATTTTCGCTGATG 3790
Db 1841 TTAAACAATATTTAAACGGGAATTTTAAACAATATTAAGCTTTTACATTTT----- 1891

Qy 3791 CGGTATTTTCTCTCGTACGATCTGTGGGTATTTTACACCGCATACAGGTGGCACTTTTC 3850
Db 1892 -----AGGTGGCACTTTTC 1905

Qy 3851 GGCGAATGTGCGGGAACCCCTATTGTTTCTAAATACATTTCAAAATATGATGATC 3910
Db 1906 GGCGAATGTGCGGGAACCCCTATTGTTTCTAAATACATTTCAAAATATGATGATC 1965

Qy 3911 CGCTCATGAGACATTAACCTGATAAATGCTTCAATAATTTTCAAAAGGAAGAGTATGA 3970
Db 1966 CGCTCATGAGACATTAACCTGATAAATGCTTCAATAATTTTCAAAAGGAAGAGTATGA 2025

Qy 3971 GTATTCAACATTTCCGCTGCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTCTCTGTTT 4030
Db 2026 GTATTCAACATTTCCGCTGCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTCTCTGTTT 2085

Qy 4031 TTGCTCACCCAGAAAACGCTGGTGAAGATGCTGAAGATCAGTTGGGTGCGACGAG 4090
Db 2086 TTGCTCACCCAGAAAACGCTGGTGAAGATGCTGAAGATCAGTTGGGTGCGACGAG 2145

Qy 4091 TGGGTTACATCGAATGGAATCTCAACAGCGGTGAAGATCTCTTGAGAGTTTTTTCGCCCGAAG 4150
Db 2146 TGGGTTACATCGAATGGAATCTCAACAGCGGTGAAGATCTCTTGAGAGTTTTTTCGCCCGAAG 2205

Qy 4151 AAGTTTTTCCAATGATGAGCACATTTTAAAGTCTGCTATGTCGCGGCTATTATTCGGTA 4210
Db 2206 AAGTTTTTCCAATGATGAGCACATTTTAAAGTCTGCTATGTCGCGGCTATTATTCGGTA 2265

Qy 4211 TTGAOCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAATGACTTGGTTG 4270
Db 2266 TTGAOCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAATGACTTGGTTG 2325

Qy 4271 AGTACTCACCGGTTCAGAAAGCATCTTACGATGCGATGACAGTAAGAGAAATTAATGCA 4330
Db 2326 AGTACTCACCGGTTCAGAAAGCATCTTACGATGCGATGACAGTAAGAGAAATTAATGCA 2385

Qy 4331 GTGCTGCCATAACCATGAGTGAATACTGCGGCCAACTTACTTCTGACAAACGATCGGAG 4390
Db 2386 GTGCTGCCATAACCATGAGTGAATACTGCGGCCAACTTACTTCTGACAAACGATCGGAG 2445

Qy 4391 GACCGAAGGAGCTAACCGCTTTTTCGCAACATGCGGGGATCATGTAACCTCGCTTGATC 4450
Db 2446 GACCGAAGGAGCTAACCGCTTTTTCGCAACATGCGGGGATCATGTAACCTCGCTTGATC 2505

Qy 4451 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGCGGTGACACCGATGCTG 4510

3192	Qy	GTGACTGGGAAAA	CCCTGGCGCTTACCCAACTTAATTCGCCTTTGCAGCACA	TCCTCCCTTTTCG	3251
1301	Db	GTGACTGGGAAAA	CCCTGGCGCTTACCCAACTTAATTCGCCTTTGCAGCACA	TCCTCCCTTTTCG	1360
3252	Qy	CCAGCTGCGTAAT	TAGCGAGAGAGCCCGCACCGAGTCGCCCTTCCACACGTTGCGCAGCC	3311	
1361	Db	CCAGCTGCGTAAT	TAGCGAGAGAGCCCGCACCGAGTCGCCCTTCCACACGTTGCGCAGCC	1420	
3312	Qy	TGAATGGCGAAT	-GGACGCGCCCTGTGTAGCGCGCATTAAGCGCGCGGTGTGTGTGTTA	3370	
1421	Db	TGAATGGCGAAT	TGGACGCGCCCTGTGTAGCGCGCATTAAGCGCGCGGTGTGTGTGTTA	1480	
3371	Qy	CGCGAGCGTGAC	CGCGCTACACTTGCACAGCCCTTAGCGCGCCCTTAGCGCGCCCTTTCGTTTCTTCCTC	3430	
1481	Db	CGCGAGCGTGAC	CGCGCTACACTTGCACAGCCCTTAGCGCGCCCTTAGCGCGCCCTTTCGTTTCTTCCTC	1540	
3431	Qy	CTTCCTTTCTCG	CCACGCTTTCGCGCGCTTTCGCCCTCAAGCTCTAAATCGCGGCGCTCCCTT	3490	
1541	Db	CTTCCTTTCTCG	CCACGCTTTCGCGCGCTTTCGCCCTCAAGCTCTAAATCGCGGCGCTCCCTT	1600	
3491	Qy	TAGGGTTCCGAT	TTTAGAGCTTTAGCGCACCTTCGACCGCAAAACCTTGAATTTGGGTGATG	3550	
1601	Db	TAGGGTTCCGAT	TTTAGAGCTTTAGCGCACCTTCGACCGCAAAACCTTGAATTTGGGTGATG	1660	
3551	Qy	GTTCACGTAGTGG	CGCATTCGCCCTGTAGACGGTTTTTCGCCCTTTGACGTTTGAGTGCCA	3610	
1661	Db	GTTCACGTAGTGG	CGCATTCGCCCTGTAGACGGTTTTTCGCCCTTTGACGTTTGAGTGCCA	1720	
3611	Qy	CGTTCTTTAATAG	TGGAGACTCTTGTTTCCAACTGGAACAAACACTCAACCTATCTCGGCTC	3670	
1721	Db	CGTTCTTTAATAG	TGGAGACTCTTGTTTCCAACTGGAACAAACACTCAACCTATCTCGGCTC	1780	
3671	Qy	ATTCTTTTGATTT	ATAAGGGATTTTCGGCATTTTCGGCTTATTTGGTTAAAAAATGAGCTGA	3730	
1781	Db	ATTCTTTTGATTT	ATAAGGGATTTTCGGCATTTTCGGCTTATTTGGTTAAAAAATGAGCTGA	1840	
3731	Qy	TTTAAACAAATAT	TTTAAACGCGAATTTTAAACAAATATTTAAAGTTTTCACAAATTTTCGCTGATG	3790	
1841	Db	TTTAAACAAATAT	TTTAAACGCGAATTTTAAACAAATATTTAAAGTTTTCACAAATTT	1891	
3791	Qy	CGGTATTTTCTC	CTTAGCGCATCTGTCGGGTATTTTCACACCGCATACAGTTGGCATTTTC	3850	
1892	Db	-----	-----AGTGGGCACATTTTC	1905	
3851	Qy	GGGGAAATGTG	CGGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATC	3910	
1906	Db	GGGGAAATGTG	CGGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATGATC	1965	
3911	Qy	CGCTCATGAGAC	CAATAACCCCTGATAAATGCTTCAATAATATGAAAGGAAGATATGA	3970	
1966	Db	CGCTCATGAGAC	CAATAACCCCTGATAAATGCTTCAATAATATGAAAGGAAGATATGA	2025	
3971	Qy	GTATTCAACATTT	CCGTGTCGCCCTTATTCCTTTTTCGGGCAATTTTCGCTTCTCTGTTT	4030	
2026	Db	GTATTCAACATTT	CCGTGTCGCCCTTATTCCTTTTTCGGGCAATTTTCGCTTCTCTGTTT	2085	
4031	Qy	TTTGCTCACCGA	AAACGCTGGTGAAGTAAAGATGCTGGAAGATCAGTTGGGTGCAACGAG	4090	
2086	Db	TTTGCTCACCGA	AAACGCTGGTGAAGTAAAGATGCTGGAAGATCAGTTGGGTGCAACGAG	2145	
4091	Qy	TGGGTTATCTG	CAACTCGAATCTCAACAGCGGTAAAGATCTCTTGAGAGTTTTTCGCCCCGGAAG	4150	
2146	Db	TGGGTTATCTG	CAACTCGAATCTCAACAGCGGTAAAGATCTCTTGAGAGTTTTTCGCCCCGGAAG	2205	
4151	Qy	AAAGTTTTTCC	AAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGGGCGGTATTTATCCGGTA	4210	
2206	Db	AAAGTTTTTCC	AAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGGGCGGTATTTATCCGGTA	2265	
4211	Qy	TTGACGCGCGG	CAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTG	4270	
2266	Db	TTGACGCGCGG	CAAGAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTG	2325	
4271	Qy	AGTACTCACAG	TCAAGAAAGCACTTACCGATGCGATGACAGTAAAGAAATTTATGCA	4330	

Db	2326		AGTACTC	CACAGT	CA	CHGAA	AAGCAT	CTT	ACGGAT	TGCAT	GACAGT	AAAGAA	TTAT	GC	2385
Qy	4331	GTGCTG	CCATAA	CCATG	AGTG	ATAA	CAC	TG	CGGCC	AACTT	TACTT	CTTG	GACAA	CGAT	CGGAG
Db	2386	GTGCTG	CCATAA	CCATG	AGTG	ATAA	CAC	TG	CGGCC	AACTT	TACTT	CTTG	GACAA	CGAT	CGGAG
Qy	4391	GACCGA	AGGAG	CTAA	CCGCT	TTTTT	TGC	AA	CATATG	GGGGAT	CA	TGTA	ACT	TGCCTT	GTATC
Db	2446	GACCGA	AGGAG	CTAA	CCGCT	TTTTT	TGC	AA	CATATG	GGGGAT	CA	TGTA	ACT	TGCCTT	GTATC
Qy	4451	GTGCGG	AAACCG	GAGCTG	GAATG	AAAGCC	ATAC	CA	AAACG	AGCGCTG	AC	CA	CCACG	ATG	CGCTG
Db	2506	GTGCGG	AAACCG	GAGCTG	GAATG	AAAGCC	ATAC	CA	AAACG	AGCGCTG	AC	CA	CCACG	ATG	CGCTG
Qy	4511	TAGCAAT	TGGCA	AAACG	TGCG	CAAACT	ATTA	CT	TGCG	AACTT	TACTT	CTG	GAAC	TACTT	CTAGCTT
Db	2566	TAGCAAT	TGGCA	AAACG	TGCG	CAAACT	ATTA	CT	TGCG	AACTT	TACTT	CTG	GAAC	TACTT	CTAGCTT
Qy	4571	GGCAACA	ATTA	TAGACT	TGGAT	TGGAG	CGGAT	AA	AGTTG	CAGG	ACCA	CTT	CTG	CGCT	TGG
Db	2626	GGCAACA	ATTA	TAGACT	TGGAT	TGGAG	CGGAT	AA	AGTTG	CAGG	ACCA	CTT	CTG	CGCT	TGG
Qy	4631	CCCTTC	CGGCTG	CTG	TGTTAT	TGCTG	ATAA	ATCT	TGAG	CGCGTG	AGCGTG	GGGCT	CTG	CGG	4690
Db	2686	CCCTTC	CGGCTG	CTG	TGTTAT	TGCTG	ATAA	ATCT	TGAG	CGCGTG	AGCGTG	GGGCT	CTG	CGG	2745
Qy	4691	GTATCAT	TG	CAGCA	CTTGG	GGCCAG	ATGGT	TA	AGCCCT	CCGCTAT	CTG	TAGT	TATCT	CA	CGA
Db	2746	GTATCAT	TG	CAGCA	CTTGG	GGCCAG	ATGGT	TA	AGCCCT	CCGCTAT	CTG	TAGT	TATCT	CA	CGA
Qy	4751	CGGGAG	T	CAGGCA	ACTATG	GATGA	AAACG	AAATAG	ACAGAT	CGCTG	AGATAG	TAGT	TGCCT	CA	4810
Db	2806	CGGGAG	T	CAGGCA	ACTATG	GATGA	AAACG	AAATAG	ACAGAT	CGCTG	AGATAG	TAGT	TGCCT	CA	2865
Qy	4811	TGATTA	AGCA	TTGGT	TAACTGT	GACG	AAAGTTT	TACT	ATATAT	TACTT	TAGAT	TGAT	TGAT	TAA	4870
Db	2866	TGATTA	AGCA	TTGGT	TAACTGT	GACG	AAAGTTT	TACT	ATATAT	TACTT	TAGAT	TGAT	TGAT	TAA	2925
Qy	4871	AACCTCA	TTTTAA	TTTAA	AAAGAT	CTAG	GTGA	AGAT	CTCTTT	TGAT	TAATCT	CT	CAT	CA	CGA
Db	2926	AACCTCA	TTTTAA	TTTAA	AAAGAT	CTAG	GTGA	AGAT	CTCTTT	TGAT	TAATCT	CT	CAT	CA	CGA
Qy	4931	AAATCC	CTTAA	CGTG	AGTTTT	CGTTCC	ATCG	TG	AGCGT	CAGAC	CCCGT	AGAAAA	AGAT	CA	AG
Db	2986	AAATCC	CTTAA	CGTG	AGTTTT	CGTTCC	ATCG	TG	AGCGT	CAGAC	CCCGT	AGAAAA	AGAT	CA	AG
Qy	4991	GATCTT	CTTG	AGAT	CTCTTTT	TCGCGG	TAA	ATCTG	CTGCTT	GCTTGC	AAACAAAA	AAAC	CA	CG	5050
Db	3046	GATCTT	CTTG	AGAT	CTCTTTT	TCGCGG	TAA	ATCTG	CTGCTT	GCTTGC	AAACAAAA	AAAC	CA	CG	3105
Qy	5051	CGCTAC	CCGCGT	GTGTTG	TTGTC	CGGAT	CA	AGAG	CTACCA	ACTCTTTT	TCCG	AGGT	TAA	5110	
Db	3106	CGCTAC	CCGCGT	GTGTTG	TTGTC	CGGAT	CA	AGAG	CTACCA	ACTCTTTT	TCCG	AGGT	TAA	3165	
Qy	5111	CTGGCT	TCAG	CAGCG	CGAGAT	ACCA	ATACT	GTCTCT	TAGT	GTAG	CCGCT	AGT	TAG	CGC	5170
Db	3166	CTGGCT	TCAG	CAGCG	CGAGAT	ACCA	ATACT	GTCTCT	TAGT	GTAG	CCGCT	AGT	TAG	CGC	3225
Qy	5171	ACCACT	TC	AA	GA	AACTCTG	TAG	CA	CCGCTT	ACAT	CTCTG	CTA	ATCTCTG	T	ACCG
Db	3226	ACCACT	TC	AA	GA	AACTCTG	TAG	CA	CCGCTT	ACAT	CTCTG	CTA	ATCTCTG	T	ACCG
Qy	5231	TGCGTC	GTG	CCAGT	GCGGAT	AGTGTG	CTT	TAC	CGGGT	TG	GACT	CA	AGACG	AT	AGT
Db	3286	TGCGTC	GTG	CCAGT	GCGGAT	AGTGTG	CTT	TAC	CGGGT	TG	GACT	CA	AGACG	AT	AGT
Qy	5291	CGGATA	AGG	CGC	AGCGGT	CGGGT									

Db	3406	GAACGACCTTACACCAACTGAGATACCTTAAGCGTGAGCTATGAGAAAGCCGACGCTTC	3465
Qy	5411	CCGAAGGAGAGAAAGCGGACAGGATATCCGGTAAGCGGAGGAGGTCGGAACAGGAGAGCGCA	5470
Db	3466	CCGAAGGAGAGAAAGCGGACAGGATATCCGGTAAGCGGAGGAGGTCGGAACAGGAGAGCGCA	3525
Qy	5471	CGAGGAGCTTCCAGGGGGAAACGCTGGTATCTTTATAGTCCCTGTGGGTTTCGCCACC	5530
Db	3526	CGAGGAGCTTCCAGGGGGAAACGCTGGTATCTTTATAGTCCCTGTGGGTTTCGCCACC	3585
Qy	5531	TCTGACTTGAGCGTCGATTTTGTGTGATGCTGTCAGGGGGCGGAGCCTATGGAAGAAACG	5590
Db	3586	TCTGACTTGAGCGTCGATTTTGTGTGATGCTGTCAGGGGGCGGAGCCTATGGAAGAAACG	3645
Qy	5591	CCAGCAACGCGGCTTTTACGGTTTCTGCGCTTTTGTGCGCTTTTGTCTCACATGTTCT	5650
Db	3646	CCAGCAACGCGGCTTTTACGGTTTCTGCGCTTTTGTGCGCTTTTGTCTCACATGTTCT	3705
Qy	5651	TTCTCGGTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCTTTTGTGAGTGAGCTGATA	5710
Db	3706	TTCTCGGTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCTTTTGTGAGTGAGCTGATA	3765
Qy	5711	CCGCTCCCGCAGCGGACGACGAGCGGACGAGTCACTGAGCGGAGCGGAGCGGAGGAGC	5770
Db	3766	CCGCTCCCGCAGCGGACGACGAGCGGACGAGTCACTGAGCGGAGCGGAGCGGAGGAGC	3825
Qy	5771	GCCCAATACGCAACCGGCTCTCCCGCGCTGCGCGGCTGCGCGGCTTCAATTAATGCAG	5822
Db	3826	GCCCAATACGCAACCGGCTCTCCCGCGCTGCGCGGCTTCAATTAATGCAG	3877
RESULT 15			
US-09-991-209-15			
; Sequence 15, Application US/09991209			
; Publication No. US20030024009A1			
; GENERAL INFORMATION:			
; APPLICANT: Dunn-Coleman, Nigel			
; APPLICANT: Langdon, Timothy			
; APPLICANT: Morse, Philip			
; TITLE OF INVENTION: Manipulation of the Phenolic Acid			
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted			
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes			
; FILE REFERENCE: G6648-2			
; CURRENT APPLICATION NUMBER: US/09/991,209			
; CURRENT FILING DATE: 2002-07-02			
; PRIOR APPLICATION NUMBER: US 60/249,608			
; PRIOR FILING DATE: 2000-11-17			
; NUMBER OF SEQ ID NOS: 97			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 15			
; LENGTH: 5338			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: pTP10-1 vector			
US-09-991-209-15			
Query Match 47.5%; Score 2768; DB 10; Length 5338;			
Best Local Similarity 96.8%; Pred. No. 0;			
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;			
Qy	2835	AAGCAGATCGTTCAACACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGCTC	2894
Db	955	AAGCAGATCGTTCAACACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGCTC	1014
Qy	2895	TTGGATGATATCATATAATTTCTGTTGAATTAGCTTAACATGTAATTAACATGT	2954
Db	1015	TTGGATGATATCATATAATTTCTGTTGAATTAGCTTAACATGTAATTAACATGT	1074
Qy	2955	AATGCAAGCTATTTATGATGAGTGGTTTTATGATTAGAGTCCCGCAATTAACATTT	3014
Db	1075	AATGCAAGCTATTTATGATGAGTGGTTTTATGATTAGAGTCCCGCAATTAACATTT	1134

Qy	3015	AATACGGATAGAAAACAAATAATATAGCGCGCAAACTAGGATAAATATATCGCGCGGCTGT	3074
Db	1135	AATACGGATAGAAAACAAATAATATAGCGCGCAAACTAGGATAAATATATCGCGCGGCTGT	1194
Qy	3075	CATCTATGTTACTAGATCGACCTCGCAGGCATCGGATCCGCGCGCCGATCGGACGTCGGGC	3134
Db	1195	CATCTATGTTACTAGATCGAATAGCTTCTAGAGCGCGCGGTGGAGC-----T	1241
Qy	3135	CCAAATTCGCCCTATAGTGAGTCGTATTAC---AATTTCACTGGCCGCTGTTTACAAAGTC	3191
Db	1242	CCAAATTCGCCCTATAGTGAGTCGTATTACGGCGGCTCACTGGCGCTGTTTACAAAGTC	1301
Qy	3192	GTGACTGGGAAAACCCCTGGCGTTTACCCAACTTAATCGCTTTTCAGCACAATCCCCCTTCG	3251
Db	1302	GTGACTGGGAAAACCCCTGGCGTTTACCCAACTTAATCGCTTTTCAGCACAATCCCCCTTCG	1361
Qy	3252	CCAGCTGGCGTAATAGCGAGAGAGCCCGCACGATCGCCCTTCCCAACAGTTTGGCGAGCC	3311
Db	1362	CCAGCTGGCGTAATAGCGAGAGAGCCCGCACGATCGCCCTTCCCAACAGTTTGGCGAGCC	1421
Qy	3312	TGAATGGCGAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGCTGTGGTGA	3370
Db	1422	TGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGCTGTGGTGA	1481
Qy	3371	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTCGCTTCTTCC	3430
Db	1482	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTCGCTTCTTCC	1541
Qy	3431	CTTCTTTCTCGCCACGTTTCGCGGCTTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	3490
Db	1542	CTTCTTTCTCGCCACGTTTCGCGGCTTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	1601
Qy	3491	TAGGTTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAACAACTTGAATTTGGGTGATG	3550
Db	1602	TAGGTTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAACAACTTGAATTTGGGTGATG	1661
Qy	3551	GTTCACTAGTGGGCAATCGCCCTGTAGAGCGTGTTCGCGCTTTTTCGAGTGGAGTCCA	3610
Db	1662	GTTCACTAGTGGGCAATCGCCCTGTAGAGCGTGTTCGCGCTTTTTCGAGTGGAGTCCA	1721
Qy	3611	CGTTCTTTAATAGTGGACTCTTGTTCGAACTGGAACAACTCAACCTATCTCGGTCT	3670
Db	1722	CGTTCTTTAATAGTGGACTCTTGTTCGAACTGGAACAACTCAACCTATCTCGGTCT	1781
Qy	3671	ATTCTTTTGATTTAAGGGATTTTGGCGATTTTCGCGCTATTTGGTTAAATAAGTGTGA	3730
Db	1782	ATTCTTTTGATTTAAGGGATTTTGGCGATTTTCGCGCTATTTGGTTAAATAAGTGTGA	1841
Qy	3731	TTTAAACAAATTTTAAACCGGAATTTTAAACAAATAATTAACGTTTTCGCTGATG	3790
Db	1842	TTTAAACAAATTTTAAACCGGAATTTTAAACAAATAATTAACGTTTTCGCTGATG	1892
Qy	3791	CGGTAATTTTCCTTACGCACTCTGCGGTATTTTACACCGCATACAGTGGCACTTTTC	3850
Db	1893	-----AGTGGCACTTTTC	1906
Qy	3851	GGGGAAATGTGCGGGAACCCCTATTTTCTTAAATACATTTCAAAATATGTATC	3910
Db	1907	GGGGAAATGTGCGGGAACCCCTATTTTCTTAAATACATTTCAAAATATGTATC	1966
Qy	3911	CGCTCATGAGACAATAACCCCTGATAAATCTTCAATAATATGAAAAGGAGATGCA	3970
Db	1967	CGCTCATGAGACAATAACCCCTGATAAATCTTCAATAATATGAAAAGGAGATGCA	2026
Qy	3971	GTATTTCAACATTTCCGTTGCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTGTTT	4030
Db	2027	GTATTTCAACATTTCCGTTGCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTGTTT	2086
Qy	4031	TTGCTCACCAGAAACGCTGTTGAAAGTAAAGATGCTGAAAGATCAGTTGGGTGACGAG	4090
Db	2087	TTGCTCACCAGAAACGCTGTTGAAAGTAAAGATGCTGAAAGATCAGTTGGGTGACGAG	2146
Qy	4091	TGGGTTACATCGAACTGATCTCAACAGCGGTAGATCCTTGGAGATTTTTCGCCCGGAG	4150

||||| 2147 TGGGTTACATCGAATCTGGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCGAAG 2206 Db
||||| 4151 AACGTTTTCCAAATGATGAGCACTTTTAAAGTTCTGTATATGCGCGGTATTAATCCGGTA 4210 Qy
||||| 2207 AACGTTTTCCAAATGATGAGCACTTTTAAAGTTCTGTATATGCGCGGTATTAATCCGGTA 2266 Db
||||| 4211 TTGACCGCGGCGAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTG 4270 Qy
||||| 2267 TTGACCGCGGCGAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTTG 2326 Db
||||| 4271 AGTACTCACCAGTACACAGAAAAGCATCTTACCGATGCGATGACAGATGAAGAAATTAATGCA 4330 Qy
||||| 2327 AGTACTCACCAGTACACAGAAAAGCATCTTACCGATGCGATGACAGATGAAGAAATTAATGCA 2386 Db
||||| 4331 GTGCTGCGCATTAACCATGAGTGATAACACTCGCGGCCAACTTTACTCTTGACAAACGATCGGAG 4390 Qy
||||| 2387 GTGCTGCGCATTAACCATGAGTGATAACACTCGCGGCCAACTTTACTCTTGACAAACGATCGGAG 2446 Db
||||| 4391 GACCGAAGGAGCTAAACCGCTTTTGGCAACAATGCGGGATCATGTAACCTGCGCTTGATC 4450 Qy
||||| 2447 GACCGAAGGAGCTAAACCGCTTTTGGCAACAATGCGGGATCATGTAACCTGCGCTTGATC 2506 Db
||||| 4451 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAACAGAGAGGTGACACCAACGATGCGCTG 4510 Qy
||||| 2507 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAACAGAGAGGTGACACCAACGATGCGCTG 2566 Db
||||| 4511 TAGCAATGGCAACAACGTTGCGCAAACTATTAACTGCGCAACTACTTTACTCTAGCTTCCC 4570 Qy
||||| 2567 TAGCAATGGCAACAACGTTGCGCAAACTATTAACTGCGCAACTACTTTACTCTAGCTTCCC 2626 Db
||||| 4571 GGCACAATTAATAGACTGGATGGAGCGGATAAAGTTGAGAGACCACTTCTGCGCTCGG 4630 Qy
||||| 2627 GGCACAATTAATAGACTGGATGGAGCGGATAAAGTTGAGAGACCACTTCTGCGCTCGG 2686 Db
||||| 4631 CCCTTCGCGTGGCTGTTTATTGCTGATAAATCTGGAGCGGTGAGCGGTGCTCGCG 4690 Qy
||||| 2687 CCCTTCGCGTGGCTGTTTATTGCTGATAAATCTGGAGCCGTTGAGCGGTGCTCGCG 2746 Db
||||| 4691 GTATCATTTGACGACCTGCGGCGCCAGATGGTAAGCCCTCCCGTATCGTATTTACTCTACACGA 4750 Qy
||||| 2747 GTATCATTTGACGACCTGCGGCGCCAGATGGTAAGCCCTCCCGTATCGTATTTACTCTACACGA 2806 Db
||||| 4751 CGGGAGTCAGGCAACTATCGATGAACGAATAGACAGATCGCTGAGATAGGTGCCTCAC 4810 Qy
||||| 2807 CGGGAGTCAGGCAACTATCGATGAACGAATAGACAGATCGCTGAGATAGGTGCCTCAC 2866 Db
||||| 4811 TGATTAAAGCAATGCTAACTCTGACACCAAGTTTACTCATATATACTTTAGATTGATTAA 4870 Qy
||||| 2867 TGATTAAAGCAATGCTAACTCTGACACCAAGTTTACTCATATATACTTTAGATTGATTAA 2926 Db
||||| 4871 AACTTCATTTTTTAATTTAAAGGATCTAGTGAAGATCCTTTTGTGATPAATCTCATGACCA 4930 Qy
||||| 2927 AACTTCATTTTTTAATTTAAAGGATCTAGTGAAGATCCTTTTGTGATPAATCTCATGACCA 2986 Db
||||| 4931 AAATCCCTTAAAGTGAAGTTTGGTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAG 4990 Qy
||||| 2987 AAATCCCTTAAAGTGAAGTTTGGTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAG 3046 Db
||||| 4991 GATCTTCTTCAGATCCCTTTTTCGCGGTAACTGCTGCTGCAACCAAAAACCAAC 5050 Qy
||||| 3047 GATCTTCTTCAGATCCCTTTTTCGCGGTAACTGCTGCTGCAACCAAAAACCAAC 3106 Db
||||| 5051 CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTTACCAACTCTTTTTCGGAAGGTAA 5110 Qy
||||| 3107 CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTTACCAACTCTTTTTCGGAAGGTAA 3166 Db
||||| 5111 CTGCTTTCAGCAGAGCGCAGATCAAAATCTGCTTCTAGTGTAGCGGTAGTAGGCC 5170 Qy
||||| 3167 CTGCTTTCAGCAGAGCGCAGATCAAAATCTGCTTCTAGTGTAGCGGTAGTAGGCC 3226 Db
||||| 5171 ACCACTTCAGAGACTCTGTAGCAGCGCTACATACCTGCTCTGCTAATCTGTTACCAG 5230 Qy

3227 ACCACTTCAGAGACTCTGTAGCAGCGCTACATACCTGCTCTGCTAATCTGTTACCAG 3286 Db
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||||| 3287 TGGCTGCTGCACTGCGGATAAAGTCTGTCTTACCCGGTTGGACTCAAGAGCATAGTTAC 3346 Db
||||| 5291 CGGATAAGCGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACACGCCACGCTTGAGC 5350 Qy
||||| 3347 CGGATAAGCGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACACGCCACGCTTGAGC 3406 Db
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||||| 3407 GAACGACCTTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCCACGCTTC 3466 Db
||||| 5411 CCAGAGGAGAGAAAGCGGAGAGATATCCCGTAAAGCGGCGGTCGGAACAGGAGAGCGCA 5470 Qy
||||| 3467 CCAGAGGAGAGAAAGCGGAGAGATATCCCGTAAAGCGGCGGTCGGAACAGGAGAGCGCA 3526 Db
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||||| 3527 CGAGGAGAGCTTCCAGGCGGAGAAACGCTGTATCTTTATAGTCTCTGCGGGTTTCGCCACC 3586 Db
||||| 5531 TCTGACTTGAGCGTTCGATTTTGTGATCTCGTCAAGGGGGCGGAGCCTATGGAAAAAAG 5590 Qy
||||| 3587 TCTGACTTGAGCGTTCGATTTTGTGATCTCGTCAAGGGGGCGGAGCCTATGGAAAAAAG 3646 Db
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||||| 3707 TTCCTGCGTTTATCCCTGATTTCTGTGATAAACCGTATTACCGCTTTTGTGAGTGTGATA 3766 Db
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||||| 3767 CCCTGCGCGCAGCCGAAACGACCGAGCGCAGCGAGTCAGTGAAGCGAGAAAGCGGAAGAGC 3826 Db
||||| 5771 GCCCAATACGCAAAACCGCTCTCCCGCGGCTTGGCGGATTCATTAATGCGAG 5822 Qy
||||| 3827 GCCCAATACGCAAAACCGCTCTCCCGCGGCTTGGCGGATTCATTAATGCGAG 3878 Db

Search completed: June 20, 2004, 15:18:02
Job time : 2242 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 10:21:08 ; Search time 21590 Seconds
(without alignments)
11687.964 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggacacaggtttccg.....tggccgattcattaatgag 5822

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hcg_hum.*

31: em_hcg_inv.*

32: em_hcg_other.*

33: em_hcg_mus.*

34: em_hcg_pln.*

35: em_hcg_rtd.*

36: em_hcg_mam.*

37: em_hcg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2892	49.7	4486	12	EVCOR116N	229589 Expression
2	2760.8	47.4	4412	12	EVCOR112N	229587 Expression
3	2755.6	47.3	5534	6	AR037157	AR037157 Sequence
4	2755.6	47.3	5534	6	AR112043	AR112043 Sequence
5	2705.8	46.5	4350	12	AF173954	AF173954 Cloning v
6	2705.8	46.5	4350	12	AF173955	AF173955 Cloning v
7	2686	46.1	4229	6	E63777	E63777 Method for
8	2683.4	46.1	3448	6	AX590988	AX590988 Sequence
9	2683.4	46.1	3448	6	AX591141	AX591141 Sequence
10	2683.4	46.1	3448	6	AX717564	AX717564 Sequence
11	2683.4	46.1	3551	12	AY122058	AY122058 Expression
12	2683.4	46.1	3711	12	AF525778	AF525778 Expression
13	2677	46.0	3033	12	CVGEM7LICF	U25272 Ligation-in
14	2677	46.0	3033	12	CVGEM7LICR	U25268 Ligation-in
15	2677	46.0	7823	12	AF041426	AF041426 Cloning v
16	2677	46.0	8658	12	AF338824	AF338824 Cloning v
17	2677	46.0	8696	12	AF379854	AF379854 Cloning v
18	2675.4	46.0	3018	6	A98767	A98767 Sequence 4
19	2671.6	45.9	3877	12	AB038599	AB038599 Cloning v
20	2671.6	45.9	6320	12	AB038600	AB038600 Cloning v
21	2668.6	45.8	4514	6	AX781452	AX781452 Sequence
22	2668.6	45.8	4514	6	AX816961	AX816961 Sequence
23	2658.4	45.7	9359	6	AX384394	AX384394 Sequence
24	2658.4	45.7	9359	6	AX473364	AX473364 Sequence
25	2654.6	45.6	2943	12	AF092940	AF092940 Cloning v
26	2654.6	45.6	3012	12	AF092546	AF092546 Cloning v
27	2641.4	45.4	2997	12	CVGEM7ZFP	X65310 Cloning vec
28	2641.4	45.4	3000	12	CVGEM5ZFP	X65308 Cloning vec
29	2641.4	45.4	3404	6	AX771236	AX771236 Sequence
30	2630.4	45.2	3485	6	AR199035	AR199035 Sequence
31	2553	43.9	6824	6	A25909	A25909 Synthetic y
32	2552	43.8	10138	12	AF187951	AF187951 Activatio
33	2552	43.8	10450	12	AF218466	AF218466 Activatio
34	2551.8	43.8	37808	6	AX001082	AX001082 Sequence
35	2550	43.8	4883	6	AR220205	AR220205 Sequence
36	2550	43.8	4883	6	AX358365	AX358365 Sequence
37	2550	43.8	11038	12	AY196826	AY196826 Piggybac
38	2549	43.8	2958	6	AX247549	AX247549 Sequence
39	2549	43.8	2958	6	AX247550	AX247550 Sequence
40	2549	43.8	2958	6	AX247551	AX247551 Sequence
41	2549	43.8	2967	12	U02449	U02449 Cloning vec
42	2547.4	43.8	4133	12	U01668	U01668 Phagemid cl
43	2542.6	43.7	2959	12	AF118920	AF118920 Cloning v
44	2538.2	43.6	10597	6	AX006825	AX006825 Sequence
45	2538.2	43.6	10597	6	AX417673	AX417673 Sequence

ALIGNMENTS

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LOCUS EVCOR116N 4486 bp DNA linear SYN 24-MAR-1994
DEFINITION Expression vector pCOR116N (modified from pCOR116 in [3]).
ACCESSION 229589
VERSION 229589.1 GI:452348
KEYWORDS ampicillin resistance; beta-lactamase; coel origin; expression
vector; nos terminator; phage f1 region; rice actin1 promoter.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 49 to 304)
AUTHORS Depicker,A., Stachel,S., Dhaese,P., Zambryski,P. and Goodman,H.M.
TITLE Napaline synthase: transcript and DNA sequence
JOURNAL J. Gen. Appl. Microbiol. 1, 561-573 (1982)

2 McElroy, D., Blowers, A.D., Jones, B. and Wu, R.
 Construction of expression vectors based on the rice actin 1 (Act1)
 5' region for use in monocot transformation
 Mol. Gen. Genet. 231 (1), 150-160 (1991)
 92092956
 MEDLINE
 1753941
 PUBMED
 REMARK
 (sites)
 3 (bases 1 to 4486)
 Liu, L., Dasgupta, I., Davies, J. and Hull, R.
 Modified expression vectors for monocot transformation toward virus
 resistance
 Unpublished
 4 (bases 1 to 4486)
 Liu, L.
 Direct Submission
 Submitted (26-JAN-1994) Liu L., John Innes Institute, Virus
 Research, Colney Lane, Norwich, United Kingdom, NR4 7UH
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 DB 49 GCAGATCGTCAACATTTGGCAATAAGTTTCTTAAGATTGAATCCTGTTGCCGCTCTT 108
 QY 2897 GCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAAATTAACATGTAA 2956
 DB 109 GCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAAATTAACATGTAA 168
 QY 2957 TGCATGATGTTATTTATGAGATGGGTTTTATGATTAGATGCCCGCAATTAACATTTAA 3016
 DB 169 TGCATGATGTTATTTATGAGATGGGTTTTATGATTAGATGCCCGCAATTAACATTTAA 228
 QY 3017 TAQCGGATAGAAACAAATATAGCGCAACTAGGATAAATTAATCGCGCGGTGTCA 3076
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3077 TCTATGTTACTAGATCGACCTGCAGCATGGGATCCGCGCGCATGCGATGCGAGTCCG 3136
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Db	2483	AGCGCAGCGGTGGGCTGAAACGGGGGGTTCGTGCAACACAGCCCGAGCTTGGAGCGAACGA	2542
Qy	5357	CTTACACCGAATCGAGATACCTACAGGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAG	5416
Db	2543	CCTACACCGAATCGAGATACCTACAGGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAG	2602
Qy	5417	GGAGAAAGCGGACAGGTATCCGTTAAGCGCAGGGTTCGGNACAGGAGAGCGCACGAGGG	5476
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Qy	5717	GCCGACGCCGAAACGACCGAGCGCAGGAGTCACTGAGCGAGGAGCGGAGAGCGGCCAA	5776
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Qy	5777	TAGCGAAACCGCTCTCCCGCGGTTGGCCGATTCAATTAATCGAG	5822
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DEFINITION	Expression vector pCOR112N (modified from pCOR112 in [2]).		
ACCESSION	Z29587		
VERSION	229587.1		
KEYWORDS	ampicillin resistance; beta-lactamase; colE1 origin; expression vector; nos terminator; phage fl region; rice actin1 promoter.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 27 to 282)		
AUTHORS	Depicker,A., Stachel,S., Dhaese,P., Zambryski,P. and Goodman,H.M.		
TITLE	Nopaline synthase: transcript mapping and DNA sequence		
JOURNAL	J. Mol. Appl. Genet. 1 (6), 561-573 (1982)		
MEDLINE	83110651		
PUBMED	7153689		
REFERENCE	2		
AUTHORS	McElroy,D., Blowers,A.D., Jones,B. and Wu,R.		
TITLE	Construction of expression vectors based on the rice actin 1 (Act1).		
JOURNAL	5' region for use in monocot transformation		
MEDLINE	Mol. Gen. Genet. 231 (1), 150-160 (1991)		
PUBMED	92092956		
REMARK	1753941		
AUTHORS	(sites)		
TITLE	3 (bases 1 to 4412)		
JOURNAL	Liu,L., Dasgupta,I., Davies,J.W. and Hull,R.		
MEDLINE	Modified vectors for monocot transformation toward virus resistance		
PUBMED	Unpublished		
REFERENCE	4 (bases 1 to 4412)		
AUTHORS	Liu,L.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-JAN-1994) Liu L., John Innes Institute, Virus		
	Research, Colney Lane, Norwich, United Kingdom, NR4 7UH		

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DB 21 ATTCTGCAGATGTTCAACATTTGGCAATAAGTTTCTTAAGATTGAATCTCTGTGCC 80
QY 2891 GGTCTTGCAGATGATATCATATAATTTCTGTGGAATTAAGCATGTAATAATAAC 2950
DB 81 CGTCTTGCAGATGATATCATATAATTTCTGTGGAATTAAGCATGTAATAATAAC 140
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DB 141 ATGTAATGATGACGTTATTATGAGATGCGTTTATGATGATGAGTCCCGCAATTATAC 200
QY 3011 ATTTAATACCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATATCGCGCGG 3070
DB 201 ATTTAATACCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATATCGCGCGG 260
QY 3071 GTGTATCTATGTTACTAGATGACCTCGCAGGATGGGATTCGCGCGCGCGATCGCAGCTC 3130
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QY 3188 CGTCGTGATCGGAAAACCTCGCGCTTACCCAACTTAATCGCTTTCGACGACATCCCTCT 3247
DB 368 CGTCGTGATCGGAAAACCTCGCGCTTACCCAACTTAATCGCTTTCGACGACATCCCTCT 427
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DB 487 AGCCTGAATGGCGAATGGACCGCCCTGTAGCGGCGCAATTAAGCGCGCGGCTGGTG 547

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1573 GATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGCGTGACACCAAGATG 1632
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4507 CCGTAGCAATGCAACAGCTTGGCCCAACTATTAACTGGCCAACTACTTACTCTAGCT 4566
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AR037157
LOCUS AR037157 5534 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5801027.
ACCESSION AR037157
VERSION AR037157.1 GI:5955013
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5534)
AUTHORS Bennett,M., May,S. and Ramsay,N.
TITLE Method of using transactivation proteins to control gene expression
in transgenic plants
JOURNAL Patent: US 5801027-A 3 01-SEP-1998;
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LOCUS 5534 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127606.
ACCESSION AR112043
VERSION AR112043.1 GI:12828891
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5534)
AUTHORS Bennett,M., May,S. and Ramsay,N.
TITLE Method of using transactivation proteins to control expression in transgenic plants
JOURNAL Patent: US 6127606-A 3 03-OCT-2000;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 47.3%; Score 2755.6; DB 6; Length 5534;
Best Local Similarity 96.3%; Pred.No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;
Qy 2840 GATCGTTCAACACTTTGGCAATAAGTTTCTTAAGATTGAATCCTGTGCGGCTTTCGG 2899
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ACCESSION AF173954
VERSION AF173954.1 GI:6002958
KEYWORDS Cloning vector pGEM-URA3
SOURCE Cloning vector pGEM-URA3
ORGANISM Cloning vector pGEM-URA3
REFERENCE 1 (bases 1 to 4350)
AUTHORS Wilson, R.B., Davis, D. and Mitchell, A.P.
TITLE Rapid hypothesis testing with *Candida albicans* through gene
disruption with short homology regions
JOURNAL J. Bacteriol. 181 (6), 1868-1874 (1999)
MEDLINE 99173911
PUBMED 10074081
REFERENCE 2 (bases 1 to 4350)
AUTHORS Wilson, R.B., Davis, D. and Mitchell, A.P.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W.
168th St., New York, NY 10032, USA
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LOCUS AF173955 5558 bp DNA circular SYN 01-OCT-1999
DEFINITION Cloning vector pGEM-HIS1, complete sequence.
ACCESSION AF173955
VERSION AF173955.1 GI:6002960
KEYWORDS Cloning vector pGEM-HIS1
SOURCE Cloning vector pGEM-HIS1
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5558)
AUTHORS Wilson, R.B., Davis, D. and Mitchell, A.P.
TITLE Rapid hypothesis testing with Candida albicans through gene
disruption with short homology regions
JOURNAL J. Bacteriol. 181 (6), 1868-1874 (1999)
MEDLINE 99173911
PubMed 14074081

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

2 (bases 1 to 5558)
Wilson, R.B., Davis, D. and Mitchell, A.P.
Direct Submission
Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W.
168th St., New York, NY 10032, USA
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ORIGIN

Query Match 46.5%; Score 2705.8; DB 12; Length 5558;
Best Local Similarity 99.9%; Pred. No. 0;
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LOCUS B63777 4229 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying the stability of genetic information in animal
cells.
ACCESSION E63777
VERSION B63777.1 GI:22553615
KEYWORDS JP 2001087000-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 4229)
Nakanishi, M. and Ikawa, Y.
AUTHORS Method for assaying the stability of genetic information in animal
TITLE Patent: JP 2001087000-A 5 03-APR-2001;
JOURNAL KK SENTAN KAGAKU GIJUTSU INCUBATION CENTER
COMMENT OS Artificial Sequence
PN JP 2001087000-A/5
PD 03-APR-2001
PF 17-SEP-1999 JP 1999264320
PI MASATO NAKANISHI, YUMI IKAWA
PC C12Q1/68, C12N5/10, C12N15/09, C12Q1/04//A61K48/00, C12N5/00; PC
C12N15/00
CC Restriction enzyme BamHI-cut site
CC Restriction enzyme SmaI-cut site
FH key Location/Qualifiers.
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Matches 2686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB TGGGAAAACCTGGCGTTACCCAACTTAATTCGCTTTCAGCACATCCCCCTTTGCCAGC 3038
QY 3257 TGGCGTAATAGCAAGAGCCCGCCAGCGATCGCCCTTCCCAACAGTTGGCAGCCGAAT 3316
DB TGGCGTAATAGCAAGAGCCCGCCAGCGATCGCCCTTCCCAACAGTTGGCAGCCGAAT 2978
QY 3317 GGCGAATGGAACGGCCCTGTAGCGGGCATTAAAGCGCGCGGTGTGGTGTACCGCA 3376
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DB TTCTCGCAGCTGCGCGCTTCCCGTCACGCTCTAATCGGGGCTCCCTTTAGGGT 2798
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QY 4697 TTGCAGCACTGGGCGCAGATGTTAGCCCTCCCGTATCGTAGTTACTACACGACGGGA 1538
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RESULT 9
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LOCUS AX591141.1
DEFINITION Sequence 6 from Patent WO02085932.
ACCESSION AX591141
VERSION AX591141.1
GI:27949651
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

artificial sequences.

REFERENCE

AUTHORS

TITLB

JOURNAL

00000000

FEATURES

AUTHORS	JOURNAL	FEATURES	source	ORIGIN
Sablon,E., van Broekhoven,A., Bosman,A., Depla,E. and Deschamps,G.	INNOGENETICS N.V. (BE)	Patent: WO 02085932-A 6 31-OCT-2002; Location/Qualifiers 1..3448 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="vector pGEMTE1sh6"	Query Match 46.1%; Score 2683.4; DB 6; Length 3448; Best Local Similarity 99.4%; Pred. No. 0; Matches 2693; Conservative 0; Mismatched 16; Indels 0; Gaps 0	
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Dd	2805	CCCACACGTTGCGCAGCTGTAATGCGCAATGGAACGGCGCCCTGTAGCGCGCAATTAAGCGC	2741	
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Db	1065	GCAACAAAAAACCACCGCTACAGCGGTGGTTGTTGCCGGATCAGAGCTACCAAC	1006
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QY	5214	GCTAATCTCTGTATCCAGTGTGCTGCTGCTGAGTGGGATTAAGTCTGTCTTACCGGGTTGA	5273
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QY	5814	TTAATGCAG 5822	
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RESULT 10
AX717564/c
LOCUS
DEFINITION Sequence 6 from Patent WO02086101.
ACCESSION AX717564
VERSION AX717564.1 GI:29890628
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Depla,E., Bosman,A., Deschamps,G., Sablon,E., Suckow,M., Samson,I.
and Verheyden,G.
TITLE Core-glycosylated hcv envelope proteins
JOURNAL Patnt: WO 02086101-A 6 31-OCT-2002;

INNOGENETICS N.V. (BE)
Location/Qualifiers
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Query Match 46.1%; Score 2683.4; DB 6; Length 3448;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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LOCUS AV122058 3551 bp DNA circular SVN 28-JUL-2002
DEFINITION Expression vector pCMH411, complete sequence.
ACCESSION AV122058
VERSION AV122058.1 GI:22001012
KEYWORDS
SOURCE Expression vector pCMH411
ORGANISM Expression vector pCMH411
REFERENCE 1 (bases 1 to 3551)
AUTHORS Hardy, C.M.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Wildlife, Pests and Diseases, CSIRO
Sustainable Ecosystems, GPO Box 284, Canberra, ACT 2601, Australia
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DEFINITION	Ligation-independent cloning vector pGEM-7zf(+)/LIC-R, complete		
ACCESSION	U25268		
VERSION	U25268.1 GI:806878		
KEYWORDS	beta-lactamase; ligation-independent cloning region; NarI restriction site.		
SOURCE	Cloning vector pGEM-7zf<+>/LIC-R		
ORGANISM	Cloning vector pGEM-7zf<+>/LIC-R		
REFERENCE	1 (bases 1 to 3033)		
AUTHORS	Haun, R.S., Serventi, I. M. and Moss, J.		
TITLE	Rapid, reliable ligation-independent cloning of PCR products using modified plasmid vectors		
JOURNAL	Biotechniques 13 (4), 515-518 (1992)		
MEDLINE	93119606		
PUBMED	1362067		


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LOCUS AF041426
DEFINITION Cloning vector pVLH-1, complete sequence.
ACCESSION AF041426
VERSION AF041426.1 GI:3025714
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 7823)
AUTHORS Deitsch,K.W. and Wellems,T.E.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-1998) LPD/NIAID, NIH, Bldg 4, Rm BI-34, Bethesda, MD 20892, USA
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Job time : 21605 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:09:12 ; Search time 1983 Seconds
(without alignments)
12472.521 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseq1990s.*

3: Geneseq2000s.*

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5: Geneseq2001bs.*

6: Geneseq2002as.*

7: Geneseq2003as.*

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9: Geneseq2003cs.*

10: Geneseq2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2683.4	46.0	3448	7	AAD50589 pGEMT18H
6	2683.4	46.0	3448	7	ABT14439 HCV envel
7	2675.4	46.0	3018	2	AAX29905 Plasmid p
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11	2668.6	45.8	4514	8	ADA94775 Plasmid p
12	2658.4	45.7	9359	6	ABK11039 pVDH636 v
13	2658.4	45.7	9359	6	ABK10687 Transform
14	2641.4	45.4	3404	8	ADA41728 Plasmid p
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17	2630.4	45.2	3485	6	AAT172813 Expressio
18	2553	43.9	4965	2	AAV18742 Complete
19	2553	43.9	5109	2	AAV13846 Complete
20	2553	43.9	6196	2	AAV13168 Complete
21	2553	43.9	6243	2	AAV13841 Complete
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C 24	2553	43.9	7379	2	AAV13176	AAV13176 Complete
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C 27	2551.8	43.8	37808	2	AAX02780	AAX02780 Vector pM
C 28	2551.4	43.8	8618	2	AAV18741	AAV18741 Complete
C 29	2550	43.8	4883	6	AAD28233	AAD28233 CMV expre
C 30	2550	43.8	7287	2	AAV02042	AAV02042 Plasmid p
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C 32	2549.4	43.8	3057	9	ADD14892	ADD14892 Phage dis
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C 34	2549	43.8	2958	4	AAV13970	AAV13970 Plasmid p
C 35	2549	43.8	2958	4	AAV13969	AAV13969 Plasmid p
C 36	2549	43.8	2958	4	AAV13971	AAV13971 Plasmid p
C 37	2549	43.8	3351	6	ABT08167	ABT08167 Recombina
C 38	2549	43.8	4754	6	ABT08175	ABT08175 Recombina
C 39	2549	43.8	4773	6	ABT08176	ABT08176 Recombina
C 40	2549	43.8	4831	6	ABT08194	ABT08194 Recombina
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C 42	2549	43.8	21329	7	AAV48562	AAV48562 ChimERIC
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ALIGNMENTS

RESULT 1

AAS20853
ID AAS20853 standard; DNA, 5822 BP.

XX AC AAS20853;

XX AC AAS20853;

XX DT 05-JUN-2002 (first entry)

XX DE Expression cassette, pFP-IRN1 useful for gene silencing.

XX KW Inhibition of gene expression; expression cassette; inverted repeat; IR;
NOS; nopaline synthase; figwort mosaic virus promoter; FMV; hsp70; PG;
plant heat shock 70; tomato; polygalacturonase; disease resistance;
flavour; nutritional characteristic; plant; gene silencing; pFP-IRN1;
regulating gene expression; mutant; ds.
XX OS Lycopersicon esculentum.
OS Agrobacterium tumefaciens.
OS Figwort mosaic virus.
OS Synthetic.
OS Chimeric.

XX FN WO200214472-A2.

XX PD 21-FBB-2002.

XX PF 14-AUG-2001; 2001WO-US025538.

XX PR 15-AUG-2000; 2000US-0225508P.

XX PR 07-AUG-2001; 2001US-00924197.

XX PA (DNAP) DNA PLANT TECHNOLOGY CORP.

XX PI Gutterson N, Oeller P;

XX DR WPI; 2002-257599/30.

XX PT Reducing the expression of a target gene in a cell, comprises expressing
in the cell an expression cassette comprising a promoter operably linked
to a sense or antisense targeting sequence and an inverted repeat of a
nopaline synthase gene.
XX PS Claim 51; Page 37-39; 39pp; English.
XX CC The present invention relates to an improved method for inhibiting the
expression of a target gene in a cell, by expressing in the cell an

expression cassette comprising a promoter operably linked to a sense or antisense targeting sequence having substantial identity to a subsequence of the target gene, and an inverted repeat (IR) of a subsequence of a NOS (neopline synthase) gene, where the IR is unrelated to the targeting sequence. The expression cassette, pPP-IRN1 is constructed using a figwort mosaic virus (FMV) promoter in which the 5'-untranslated leader (5'-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato polygalacturonase (PG) gene and an IR of the terminator of the Agrobacterium tumefaciens NOS gene. The method is useful for regulating expression of endogenous genes and transgenes, e.g. to regulate expression of endogenous plant phenotypes such as disease resistance, flavour, protein or nutritional characteristics. The improved gene silencing construct is used in functional genomics to determine the effect of regulating gene expression of a selected endogenous gene or transgene. The method is simple and rapid, and is suitable for high-throughput studies. Multiple transgenic constructs all containing the same repeat element can be silenced at the same time, since the initial silencing trigger mediated through the inverted repeat region will apply to all of the transcripts. The present sequence represents the expression cassette, pPP-IRN1

SQ Sequence 5822 BP; 1689 A; 1275 C; 1292 G; 1566 T; 0 U; 0 Other;

Query Match 100.0%; Score 5822; DB 6; Length 5822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1021	GTAATCTGTCACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAGAAATGCTGCA	1080
QY	1081	GAAATCTGTTAGGCGCACTACCAAAAGCACTTTGGCTTTATTGCAAAAGATAAGCAGAT	1140
DB	1081	GAAATCTGTTAGGCGCACTACCAAAAGCACTTTGGCTTTATTGCAAAAGATAAGCAGAT	1140
QY	1141	CCTCTAGTACAGTGGGGAACAAATTAACGTTGAAAGAGCTGTCTCTGACAGCCCACTCA	1200
DB	1141	CCTCTAGTACAGTGGGGAACAAATTAACGTTGAAAGAGCTGTCTCTGACAGCCCACTCA	1200
QY	1201	CTAATCGGTATGACGAAACGAGTACGACCAACAAAGAAATTCCTCTATATAAGAGGCA	1260
DB	1201	CTAATCGGTATGACGAAACGAGTACGACCAACAAAGAAATTCCTCTATATAAGAGGCA	1260
QY	1261	TTCAATTTCCCAATTTGAAGGACACAGAAAAATTTGCTACATTTGTTTCAAAAATAT	1320
DB	1261	TTCAATTTCCCAATTTGAAGGACACAGAAAAATTTGCTACATTTGTTTCAAAAATAT	1320
QY	1321	TATTCATTTATTTGTCAGCTTTCAAACTCTTTGTTCTTGTGTTGTTGATGAGAAATAT	1380
DB	1321	TATTCATTTATTTGTCAGCTTTCAAACTCTTTGTTCTTGTGTTGTTGATGAGAAATAT	1380
QY	1381	AAAAACCATGTTCTTAAAAACAGAAATTTATCTCTCAAGCAAAATCACCTTTTCAGGTCCA	1440
DB	1381	AAAAACCATGTTCTTAAAAACAGAAATTTATCTCTCAAGCAAAATCACCTTTTCAGGTCCA	1440
QY	1441	TGCAGATCTTCTAATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAAAATTTCA	1500
DB	1441	TGCAGATCTTCTAATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAAAATTTCA	1500
QY	1501	GACTACAAAGATAGAGGCTTTGGATTTGTTGATAGTTGTTCAAAATTTAGTTGTTGA	1560
DB	1501	GACTACAAAGATAGAGGCTTTGGATTTGTTGATAGTTGTTCAAAATTTAGTTGTTGA	1560
QY	1561	GGAGGAGGAATCTCAATGCGAATGCAAGTATGTTGGCCCAAGTTCTTCCAAAATTAAT	1620
DB	1561	GGAGGAGGAATCTCAATGCGAATGCAAGTATGTTGGCCCAAGTTCTTCCAAAATTAAT	1620
QY	1621	AAATCACTGCCATGCGAGGATGCCAACCGGCTTTAACTTTCTGGAAATTCGAAAATTTG	1680
DB	1621	AAATCACTGCCATGCGAGGATGCCAACCGGCTTTAACTTTCTGGAAATTCGAAAATTTG	1680
QY	1681	AAAGTGAATTAATCTAAAGATGAAATGCAACAAATTTCAATCAAAATTTGATGCTATGC	1740
DB	1681	AAAGTGAATTAATCTAAAGATGAAATGCAACAAATTTCAATCAAAATTTGATGCTATGC	1740
QY	1741	ACTAATGTTGTTAGCTTTCAAAATTTGATGATGATGCTTTGCAAAAGAGCCCAATCTGAT	1800
DB	1741	ACTAATGTTGTTAGCTTTCAAAATTTGATGATGATGCTTTGCAAAAGAGCCCAATCTGAT	1800

[illegible]

PD 09-AUG-1996.
XX
PF 24-MAY-1995; 95CA-02150039.
XX
PR 08-FEB-1995; 95GB-00002456.
XX
PA (UYWA-) UNIV WARWICK.
XX
PI Bennett M, May S, Ramsay N;
XX
DR WPI; 1996-486150/49.
XX
PT Control of genes in transgenic plants - using an upstream activating
PT sequence activated by a transactivating protein expressed using a
PT separate promoter.
XX
PS Example; Fig 5P; 48pp; English.
XX
CC Reporter plasmid pUMIGIT (AAV43137), or pUAS Minimal promoter Gus Int.
CC Terminator, contains a beta-glucuronidase (GUS) reporter gene under the
CC control of the 468 cauliflower-mosaic virus minimal promoter and 10
CC synthetic 17-bp GAL4 binding sites. The upstream activating sequence
CC (UAS) of pUMIGIT is activatable by yeast transactivating protein GAL4. In
CC a novel method for controlling gene expression, a first transgenic plant
CC carrying a gene encoding a desired phenotype (herbicide resistance of
CC polyhydroxybutyrate prodn.) operatively linked to a UAS recognition site
CC is pollinated by a second transgenic plant carrying Gal4 DNA (see also
CC AAV43136). The transgene is fully expressed in F1 hybrid plants but
CC segregates apart in subsequent generations, improving environmental
CC safety
XX
SQ Sequence 5534 BP; 1400 A; 1355 C; 1387 G; 1363 T; 0 U; 29 Other;
Query Match 47.4%; Score 2757.2; DB 2; Length 5534;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2891; Conservative 0; Mismatches 37; Indels 74; Gaps 4;
Qy 2840 GATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCTTGTGCGCGTCTTGGC 2899
Db 2366 GATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCTTGTGCGCGTCTTGGC 2425
Qy 2900 ATGATTATCATATAATTTCTGTGTAATACGTTTAAGCATGTAATAATTAACATGTAATGC 2959
Db 2426 ATGATTATCATATAATTTCTGTGTAATACGTTTAAGCATGTAATAATTAACATGTAATGC 2485
Qy 2960 ATGAGTTATTTATGAGATGGTTTTTTATGATTAGATGCGCAATTATACATTTAATAC 3019
Db 2486 ATGAGTTATTTATGAGATGGTTTTTTATGATTAGATGCGCAATTATACATTTAATAC 2545
Qy 3020 GCGATAGAAAACAAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGTCATCT 3079
Db 2546 GCGATAGAAAACAAATATAGCGCGCAAACTAGGATAAATTTATCGCGCGGTGTCATCT 2605
Qy 3080 ATGTTACTAGATCGACC-----TGCAAGCATGGGATCGCGCGCGCATGC 3124
Db 2606 ATGTTACTAGATCGNNNGAATTCGATATCAAGCTTATCGATACCGTCACTCGAGCGGG 2665
Qy 3125 GACGTGCGGCGCCCAATTCGCCCTATAGTGAATGCTATTAC---AATTCATCGCGCGTCTT 3181
Db 2666 GGCCCGGTACCAATTCGCCCTATAGTGAATGCTATTACGCGCGGTCACTGCGCGTCTT 2725
Qy 3182 TTACAACTGCTGACTGGGAAAACCCCTGCGGTACCCAACTTAATTCGCTTTCGAGCACAT 3241
Db 2726 TTACAACTGCTGACTGGGAAAACCCCTGCGGTACCCAACTTAATTCGCTTTCGAGCACAT 2785
Qy 3242 CCCCTTTTCGCGCTGCTGAGTAAATAGCGAGGCGCCGCAATTCGCGCTTCCCAACAG 3301
Db 2786 CCCCTTTTCGCGCTGCTGAGTAAATAGCGAGGCGCCGCAATTCGCGCTTCCCAACAG 2845
Qy 3302 TTGCGCAGCTGAATGGCGAAT-GGACGCGCGCTGTAGCGCGCAATTAAGCGCGCGGT 3360
Db 2846 TTGCGCAGCTGAATGGCGAATGGGACGCGCGCTGTAGCGCGCAATTAAGCGCGCGGT 2905

Qy 3361 GTGGTGGTTTACGGCAGCGGTGACCGCTACACTTGGCAGCGCGCTAGCGCGCGCTTCTTTC 3420
Db 2906 GTGGTGGTTTACGGCAGCGGTGACCGCTACACTTGGCAGCGCGCTAGCGCGCGCTTCTTTC 2965
Qy 3421 GCTTTCTTCCCTTCTCTCGCCACAGTTGCGCGCGCTTCCCGCTCAAGCTCTAAATCGG 3480
Db 2966 GCTTTCTTCCCTTCTCTCGCCACAGTTGCGCGCGCTTCCCGCTCAAGCTCTAAATCGG 3025
Qy 3481 GGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGAT 3540
Db 3026 GGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGAT 3085
Qy 3541 TTGGGTGATGGTTCACTAGTAGGGCCATCGCCCTGATAGACGGTTTTCGCGCTTGAAG 3600
Db 3086 TAGGGTGAATGGTTCACTAGTAGGGCCATCGCCCTGATAGACGGTTTTCGCGCTTGAAG 3145
Qy 3601 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAAACAACACTCAACCT 3660
Db 3146 TTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAAACAACACTCAACCT 3205
Qy 3661 ATCTCGGTCTATTTCTTTGATTTATAAGGGATTTTTCGGATTTTCGGCTTATTTGTTAAAA 3720
Db 3206 ATCTCGGTCTATTTCTTTGATTTATAAGGGATTTTTCGGATTTTTCGGCTTATTTGTTAAAA 3265
Qy 3721 AATGAGCTGATTTACAAATATTTAAACGGAAATTTTACAAATATTTACAAATTTTACAAT 3780
Db 3266 AATGAGCTGATTTACAAATATTTAAACGGAAATTTTAAACAAATATTTAAACGGCTTACAAT 3325
Qy 3781 TCGCCTGATGCGGTATTTTCTCTTACGATCTGTGCGGTATTTTCACACCGCATACAGT 3840
Db 3326 T-----AGGT 3330
Qy 3841 GGCACTTTTCGGGAAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3900
Db 3331 GGCACTTTTCGGGAAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCA 3390
Qy 3901 AATATGATTCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATTTGAAAAAGG 3960
Db 3391 AATATGATTCGCTCATGAGACAATAAACCCTGATAAATGCTTCAATAATTTGAAAAAGG 3450
Qy 3961 AAGAGTATGAGTATTTCAACATTTCCGTGCGCCCTTATTTCCCTTTTTCGGCGATTTTCG 4020
Db 3451 AAGAGTATGAGTATTTCAACATTTCCGTGCGCCCTTATTTCCCTTTTTCGGCGATTTTCG 3510
Qy 4021 CTTCTCTTTTGTCTCAACCGAAGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGTTG 4080
Db 3511 CTTCTCTTTTGTCTCAACCGAAGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGTTG 3570
Qy 4081 GGTCACAGAGTGGGTTATCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTCGAGAGTTT 4140
Db 3571 GGTGCAAGAGTGGGTTATCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTCGAGAGTTT 3630
Qy 4141 GCGCCGGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTA 4200
Db 3631 GCGCCGGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTA 3690
Qy 4201 TTATCCCTTATTTGAGCGCGGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAT 4260
Db 3691 TTATCCCTTATTTGAGCGCGGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAT 3750
Qy 4261 GACTTGGTTGAGTACTCAACAGTCAACAGAAAGCATCTTACGGATGGCATGACAGTAAGA 4320
Db 3751 GACTTGGTTGAGTACTCAACAGTCAACAGAAAGCATCTTACGGATGGCATGACAGTAAGA 3810
Qy 4321 GAAATATCAGTGTGCTCAATACATGATGATTAACACTCGCGCGCAACTTACTTCTGACA 4380
Db 3811 GAAATATCAGTGTGCTCAATACATGATGATTAACACTCGCGCGCAACTTACTTCTGACA 3870
Qy 4381 ACGATCGAGGACCGGAAGAGCTAACCGCTTTTTCGACAAACATCGGGGATCATGTAAT 4440
Db 3871 ACGATCGAGGACCGGAAGAGCTAACCGCTTTTTCGACAAACATCGGGGATCATGTAAT 3930
Qy 4441 GCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGGTGACACC 4500

Db 3931 |||||CGCCTTGATCGTTGGGAACCGGAGCTGATGAGACCCATACCAACGACGAGCGGTGACACC||| 3990
Qy 4501 ACAGTGCCTGFPAGCAATGGCAACAACTGTCGGCAAACTATTAACTGCGCAACTACTTACT 4560
Db 3991 ACAGTGCCTGFPAGCAATGGCAACAACTGTCGGCAAACTATTAACTGCGCAACTACTTACT 4050
Qy 4561 CTAGCTTCCGGCAACAACTTAATAGACTGAGTGGAGGGGAGTAAAGTTGACGAGCACTT 4620
Db 4051 CTAGCTTCCGGCAACAACTTAATAGACTGAGTGGAGGGGAGTAAAGTTGACGAGCACTT 4110
Qy 4621 CTGCGCTCGGCGCTTCGCGCTGCTGCTTTATTCCTGATTAATCTGAGCGCGGTGAGCGT 4680
Db 4111 CTGCGCTCGGCGCTTCGCGCTGCTGCTTTATTCCTGATTAATCTGAGCGCGGTGAGCGT 4170
Qy 4681 GGGTCTCGCGGTATCATTTGACAGCACTCGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4740
Db 4171 GGGTCTCGCGGTATCATTTGACAGCACTCGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT 4230
Qy 4741 ATCTACAGGACGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGAT 4800
Db 4231 ATCTACAGGACGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGAT 4290
Qy 4801 GGTCCCTCACTGATTAAAGCATTTGTAACTGTCAGACCAAGTTTACTCATATATATCTTTAG 4860
Db 4291 GGTCCCTCACTGATTAAAGCATTTGTAACTGTCAGACCAAGTTTACTCATATATATCTTTAG 4350
Qy 4861 ATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTTTGATAAT 4920
Db 4351 ATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTTTGATAAT 4410
Qy 4921 CTATGACCAAAATCCCTTAAGTGAAGTTTTCGTTCTCACTGAGCGTCAGACCCCGTAGAA 4980
Db 4411 CTATGACCAAAATCCCTTAAGTGAAGTTTTCGTTCTCACTGAGCGTCAGACCCCGTAGAA 4470
Qy 4981 AAGATCAAGGATCTTCTTGAGATCTCTTTTCTGCGCGTAATCTGCTGTGCAACA 5040
Db 4471 AAGATCAAGGATCTTCTTGAGATCTCTTTTCTGCGCGTAATCTGCTGTGCAACA 4530
Qy 5041 AAAAAACACCGCTACCAAGCGGTGGTTTGTTCGGGATCAAGACTACCAACTCTTTT 5100
Db 4531 AAAAAACACCGCTACCAAGCGGTGGTTTGTTCGGGATCAAGACTACCAACTCTTTT 4590
Qy 5101 CCGAAGTAACTGGCTTCAGCAGAGCGCAGATACCAATATCTGCTCTAGTGTAGCGG 5160
Db 4591 CCGAAGTAACTGGCTTCAGCAGAGCGCAGATACCAATATCTGCTCTAGTGTAGCGG 4650
Qy 5161 TAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATC 5220
Db 4651 TAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATC 4710
Qy 5221 CTGTTACAGTGGCTGCTCCAGTGGCGATTAAGTGTGTTCTTACCGGGTTGGACTCAAGA 5280
Db 4711 CTGTTACAGTGGCTGCTCCAGTGGCGATTAAGTGTGTTCTTACCGGGTTGGACTCAAGA 4770
Qy 5281 CGATAGTTACCGGATTAAGCGCCAGCGTTCGGCTGGAACGGGGGTTCGTGCACACAGCCC 5340
Db 4771 CGATAGTTACCGGATTAAGCGCCAGCGTTCGGCTGGAACGGGGGTTCGTGCACACAGCCC 4830
Qy 5341 AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAGC 5400
Db 4831 AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATGAGAAGC 4890
Qy 5401 GCCACGCTTCCGAAGGAGAAAGCGGATATCCGGTATCCGGTATCCGGTTCGGGAACA 5460
Db 4891 GCCACGCTTCCGAAGGAGAAAGCGGATATCCGGTATCCGGTATCCGGTTCGGGAACA 4950
Qy 5461 GCAGAGCGCAGGAGCTTCCAGGGGGAACCGCTGATCTTTATAGTCTCTCTCGGG 5520
Db 4951 GCAGAGCGCAGGAGCTTCCAGGGGGAACCGCTGATCTTTATAGTCTCTCTCGGG 5010
Qy 5521 TTTCGCCACCTCTGACTTGAAGCTCGATTTTGTGATGCTGCTCAGGGGGCGGAGCTA 5580

Db 5011 TTTCGCCACCTCTGACTTGAGCGTGCATTTTGTGATGCTCGTCAGGGGGCGGAGCCCTA 5070
Qy 5581 TGGAAAAACGCGACGAAACGCGGCCCTTTTACGGTTCCTTGGCCTTTTGTGCGCTTTTGTCT 5640
Db 5071 TGGAAAAACGCGACGAAACGCGGCCCTTTTACGGTTCCTTGGCCTTTTGTGCGCTTTTGTCT 5130
Qy 5641 CACATGTTCTTCTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGCTTTGAG 5700
Db 5131 CACATGTTCTTCTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGCTTTGAG 5190
Qy 5701 TGAGCTGATACCGCTCGCGCCAGCAACGACCGAGCGCAGCGAGTCAAGTGAAGCGAGAA 5760
Db 5191 TGAGCTGATACCGCTCGCGCCAGCAACGACCGAGCGCAGCGAGTCAAGTGAAGCGAGAA 5250
Qy 5761 GCGAAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCGCGATTCATTAATGC 5820
Db 5251 GCGAAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCGCGATTCATTAATGC 5310
Qy 5821 AG 5822
Db 5311 AG 5312

RESULT 3
AAH25896/C
ID AAH25896 standard; DNA; 4229 BP.
XX AAH25896;
AC AC
XX XX
DT 24-AUG-2001 (first entry)
XX XX
DB Genetic information stability related oligonucleotide #5.
XX XX
KW Genetic information stability measurement; drug resistance; ds.
XX XX
OS Synthetic.
PN JP2001087000-A.
XX XX
PD 03-APR-2001.
XX XX
PF 17-SEP-1999; 99JP-00264320.
PR 17-SEP-1999; 99JP-00264320.
XX XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX XX
PS WPI; 2001-360322/38.
CC Measurement of stability of genetic information in an animal cell,
PT comprises introducing a vector having a gene resistant to a first drug
PT and a gene sensitive to a second drug, to an animal cell.
XX XX
PS Disclosure; Page 8-9; 12pp; Japanese.
XX XX
CC The present invention describes a method for the measurement of stability
CC of genetic information in an animal cell in which a vector having a gene
CC resistant to a first drug and a gene sensitive to a second drug is
CC introduced into the animal cell. This can be used for the measurement of
CC stability of genetic information in an animal cell. The present sequence
CC is an oligonucleotide used in the exemplification of the invention
XX XX
SQ Sequence 4229 BP; 1108 A; 1004 C; 1036 G; 1081 T; 0 U; 0 Other;

Query Match 46.1%; Score 2686; DB 4; Length 4229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3137 AATTGCGCCCTATAGTGTGATTCATTAATTCATTCGCGCGCTGTTTACAAAGTCTGTCAC 3196
Db 3157 AATTGCGCCCTATAGTGTGATTCATTAATTCATTCGCGCGCTGTTTACAAAGTCTGTCAC 3098
Qy 3197 TGGGAAAAACCTCGCGTTTACCACCACTTAATCGCCTTGCAGCACATCCCTTTCGCCAGC 3256

|||||
3097 TGGGAAACCTTGGCGTTACCGAATTAAATCGCCTTGGCGACATCCCCCTTTCCGACG 3038
QY
3257 TGGCGTAAATAGCGAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCGCTGAAT 3316
Db
3037 TGGCGTAAATAGCGAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCGCTGAAT 2978
QY
3317 GGCGAATGGAAGCGCGCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGTAGCGGCA 3376
Db
2977 GGCGAATGGAAGCGCGCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGTAGCGGCA 2918
QY
3377 CGGTGACCGCTACACTTCCGACGCGCCTAGCGCCCGCTCCCTTTCGCTTCTTCCCTTCCT 3436
Db
2917 GCGTGACCGCTACACTTCCGACGCGCCTAGCGCCCGCTCCCTTTCGCTTCTTCCCTTCCT 2858
QY
3437 TTCTCGCCACGTTGCGCGCTTTCGCGTCAAGCTCTAAATCGCGGGCTCCCTTTPAGGGT 3496
Db
2857 TTCTCGCCACGTTGCGCGCTTTCGCGTCAAGCTCTAAATCGCGGGCTCCCTTTPAGGGT 2798
QY
3497 TCCGATTTAGAGCTTTACGGCACTTCGACCGCGCAAAAACCTTGATTTGGGTGATGGTTAC 3556
Db
2797 TCCGATTTAGAGCTTTACGGCACTTCGACCGCGCAAAAACCTTGATTTGGGTGATGGTTAC 2738
QY
3557 GTAGTGGCCATCGCCCTGTAGAGCGTTTTCGCCCTTTGAGCGTTGAGTCCAGTTCT 3616
Db
2737 GTAGTGGCCATCGCCCTGTAGAGCGTTTTCGCCCTTTGACGTTGGAGTCCAGTTCT 2678
QY
3617 TTAATAGTGGACTCTTGTTCCAAACCTGGAACAACACTCAACCCCTATCTCGGTCTATTCTT 3676
Db
2677 TTAATAGTGGACTCTTGTTCCAAACCTGGAACAACACTCAACCCCTATCTCGGTCTATTCTT 2618
QY
3677 TTGATTTAAGAGGATTTGCGGATTCGCGCTATTTGGTTAAAAAATGAGCTGATTTAAC 3736
Db
2617 TTGATTTAAGAGGATTTGCGGATTTGCGGCTATTTGGTTAAAAAATGAGCTGATTTAAC 2558
QY
3737 AAATAATTAACCGCAATTTTAAACAAATATTAACGTTTACAAATTCGCTCGATCGGTAT 3796
Db
2557 AAATAATTAACCGCAATTTTAAACAAATATTAACGTTTACAAATTCGCTCGATCGGTAT 2498
QY
3797 TTTCTCTTACGCACTCTGTGGGTAATTTACACCGCATACAGGTGGCACTTTTCGGGAA 3856
Db
2497 TTTCTCTTACGCACTCTGTGGGTAATTTACACCGCATACAGGTGGCACTTTTCGGGAA 2438
QY
3857 ATGTGCGGGAAACCCCTATTTGTTTATTTCTAAATACATTCAAATATGTATCGCTCA 3916
Db
2437 ATGTGCGGGAAACCCCTATTTGTTTATTTCTAAATACATTCAAATATGTATCGCTCA 2378
QY
3917 TGAGACAATAACCTGTATAATGCTTCAATAATTTGAAAAGGAAGATGAGTATTC 3976
Db
2377 TGAGACAATAACCTGTATAATGCTTCAATAATTTGAAAAGGAAGATGAGTATTC 2318
QY
3977 AACATTTCCGTGTGCGCCCTTATTCCTTTTTCGGGCAATTTGCTTCCTGTTTTCGTC 4036
Db
2317 AACATTTCCGTGTGCGCCCTTATTCCTTTTTCGGGCAATTTGCTTCCTGTTTTCGTC 2258
QY
4037 ACCCGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGTGGGTT 4096
Db
2257 ACCCGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGTGGGTT 2198
QY
4097 ACATCGAATGATCTCAACAGCGTAAAGATCTTTGAGAGTTTTCGCCCGCAAGACGTT 4156
Db
2197 ACATCGAATGATCTCAACAGCGTAAAGATCTTTGAGAGTTTTCGCCCGCAAGACGTT 2138
QY
4157 TTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATFGACG 4216
Db
2137 TTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATFGACG 2078
QY
4217 CCGGGCAAGAGAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACT 4276
Db
2077 CCGGGCAAGAGAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACT 2018
QY
4277 CACCAAGTCACAGAAAGCACTTACGATGGCATGACAGTAAAGAAATTTATGACGTGCTG 4336
|||||

2017 CACCAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATTTATGCAGTGCTG 1958
QY
4337 CCATAACCATGAGTGATAAACACTGCGGCAACTTTACTTCTTGACAACAGATCGGAGGACGA 4396
Db
1957 CCATAACCATGAGTGATAAACACTGCGGCAACTTTACTTCTTGACAACAGATCGGAGGACGA 1898
QY
4397 AGGAGCTAAACCGCTTTTTCACACATGCGGGATCATGTAACTCGCTTGTATGCTTGGG 4456
Db
1897 AGGAGCTAAACCGCTTTTTCACACATGCGGGATCATGTAACTCGCTTGTATGCTTGGG 1838
QY
4457 AACCGGAGCTGAATGAAGCCCATACCAACGACGAGCGTGACACCAAGATGCTGTAGCAA 4516
Db
1837 AACCGGAGCTGAATGAAGCCCATACCAACGACGAGCGTGACACCAAGATGCTGTAGCAA 1778
QY
4517 TGGCAAAACGTTGCGCAAACTATTAACCTGCGCAACTTACTTCTCTAGCTTCCCGGCAAC 4576
Db
1777 TGGCAAAACGTTGCGCAAACTATTAACCTGCGCAACTTACTTCTCTAGCTTCCCGGCAAC 1718
QY
4577 AATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGGACCACTTCTGCGCTCGGCCCTTC 4636
Db
1717 AATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGGACCACTTCTGCGCTCGGCCCTTC 1658
QY
4637 CGGCTGGCTGCTTATTTCTGATTAATCTGGAGCGGCTGAGCGTGGGTCTCGCGGTATCA 4696
Db
1657 CGGCTGGCTGCTTATTTCTGATTAATCTGGAGCGGCTGAGCGTGGGTCTCGCGGTATCA 1598
QY
4697 TTGACGACTGCGGCGAGATGTTAAGCTTCCGCTATCGTATCTATACACGCGGGA 4756
Db
1597 TTGACGACTGCGGCGAGATGTTAAGCTTCCGCTATCGTATCTATACACGCGGGA 1538
QY
4757 GTGAGGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCACTGATTA 4816
Db
1537 GTGAGGCAACTATGATGAACGAAATAGACAGATCGCTGAGATAGTGCCTCACTGATTA 1478
QY
4817 AGCATTTGTTAACTGTGACCAAGTTTACTCATATATATCTTTAGATTTGATTTAAACCTTC 4876
Db
1477 AGCATTTGTTAACTGTGACCAAGTTTACTCATATATATCTTTAGATTTGATTTAAACCTTC 1418
QY
4877 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGAATATCTCATGACCAAAATCC 4936
Db
1417 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTGAATATCTCATGACCAAAATCC 1358
QY
4937 CTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTT 4996
Db
1357 CTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGGATCTT 1298
QY
4997 CTTGAGATCTCTTTTCTGCGGTAATCTGCTGCTTGCATAACAAAACCAACCGCTAC 5056
Db
1297 CTTGAGATCTCTTTTCTGCGGTAATCTGCTGCTTGCATAACAAAACCAACCGCTAC 1238
QY
5057 CAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGGTAACTGGCT 5116
Db
1237 CAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCGAAAGGTAACTGGCT 1178
QY
5117 TCAGCAGAGCGCAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCCACCACT 5176
Db
1177 TCAGCAGAGCGCAGATACCAATCTGCTTCTAGTGTAGCGGTAGTTAGGCCACCACT 1118
QY
5177 TCAGAACTCTGTAGCAGCGCTCATCATCTGCTCTGCTAACTCTTTTACAGGTGGGCTG 5236
Db
1117 TCAGAACTCTGTAGCAGCGCTCATCATCTGCTCTGCTAACTCTTTTACAGGTGGGCTG 1058
QY
5237 CTGCGAGTGGCGATAAGTGTGTTTACCGGTTTGGACTCAAGAGATAGTTACCGGATA 5296
Db
1057 CTGCGAGTGGCGATAAGTGTGTTTACCGGTTTGGACTCAAGAGATAGTTACCGGATA 998
QY
5297 AGGCGCAGCGGTGCGGCTGAACCGGGGTTGTCGACACAGCCAGCTTGGAGCGCAACGA 5356
Db
997 AGGCGCAGCGGTGCGGCTGAACCGGGGTTGTCGACACAGCCAGCTTGGAGCGCAACGA 938
QY
5357 CTTACACCGCAACTGAGATACCTTACAGCGTGTAGCTATGAGAAAGCGCCACGCTTCCGGAAG 5416
Db
937 CTTACACCGCAACTGAGATACCTTACAGCGTGTAGCTATGAGAAAGCGCCACGCTTCCGGAAG 878

3894 ACATTCAATATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATTG 3953
|||||
2205 ACATTCAATATGATCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATTG 2146
|||||
3954 AAAAGGAAGATGAGTATTCAACATTTCGTGTCGCCCTTATTCCTTTTTCGCGC 4013
|||||
2145 AAAAGGAAGATGAGTATTCAACATTTCGTGTCGCCCTTATTCCTTTTTCGCGC 2086
|||||
4014 ATTTTGCCTTCCTGTTTTCCTCACCCAGAAACCGTGTGTAAGATGCTGAAGA 4073
|||||
2085 ATTTTGCCTTCCTGTTTTCCTCACCCAGAAACCGTGTGTAAGATGCTGAAGA 2026
|||||
4074 TCAGTTGGGTGACAGTGGGTATCATCGAATGATCTCAACAGCGGTAGATCCTTGA 4133
|||||
2025 TCAGTTGGGTGACAGTGGGTATCATCGAATGATCTCAACAGCGGTAGATCCTTGA 1966
|||||
4134 CAGTTTTCGCCGCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGGG 4193
|||||
1965 GAGTTTTCGCCGCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGGG 1906
|||||
4194 CGCGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGATACACTATTC 4253
|||||
1905 TACACTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCGGCGGTATTC 1846
|||||
4254 TCAGATGACTTGGTTGAGTACTCACAGTCTACAGAAAGCATCTTACGATGGGATGAC 4313
|||||
1845 TCAGATGACTTGGTTGAGTACTCACAGTCTACAGAAAGCATCTTACGATGGGATGAC 1786
|||||
4314 AGTAAGAGAAATTATGCACTGCTGCCATAACCATGATGATTAACACTGCGGCCCACTTACT 4373
|||||
1785 AGTAAGAGAAATTATGCACTGCTGCCATAACCATGATGATTAACACTGCGGCCCACTTACT 1726
|||||
4374 TCTGACAAACGATCGGAGAACCGAAGAGCTAACCGCTTTTTCGCAACAACATGGGGGATCA 4433
|||||
1725 TCTGACAAACGATCGGAGAACCGAAGAGCTAACCGCTTTTTCGCAACAACATGGGGGATCA 1666
|||||
4434 TGTAAGTCTGCTGATGCTGCGGACCGGAGCTGAATGCAAGCCATACCAACGAGCGG 4493
|||||
1665 TGTAAGTCTGCTGATGCTGCGGACCGGAGCTGAATGCAAGCCATACCAACGAGCGG 1606
|||||
4494 TGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACTGCGGCAACT 4553
|||||
1605 TGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACTGCGGCAACT 1546
|||||
4554 ACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGAGTGGAGCGGATAAAGTTGCAAG 4613
|||||
1545 ACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGAGTGGAGCGGATAAAGTTGCAAG 1486
|||||
4614 ACCACTTCTGCGTCCGCGCTTCCGCGTGGCTGTTTATTTGCTGATTAATCTGGAGCGG 4673
|||||
1485 ACCACTTCTGCGTCCGCGCTTCCGCGTGGCTGTTTATTTGCTGATTAATCTGGAGCGG 1426
|||||
4674 TGAGCGTGGGTCTCGCGTATCATTTGACAGACTGGGGCGAGTGAAGCCCTCCCGTAT 4733
|||||
1425 TGAGCGTGGGTCTCGCGTATCATTTGACAGACTGGGGCGAGTGAAGCCCTCCCGTAT 1366
|||||
4734 CGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATGCG 4793
|||||
1365 CGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATGCG 1306
|||||
4794 TGAGTAGTTCGCTCAGCTGATTAAGCATTTGATGTTACTGTGACCCAGATTTACTCATATAT 4853
|||||
1305 TGAGTAGTTCGCTCAGCTGATTAAGCATTTGATGTTACTGTGACCCAGATTTACTCATATAT 1246
|||||
4854 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 4913
|||||
1245 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 1186
|||||
4914 TGATAATCTCATGACCAAAATCCCTTAAACGAGTTTTCCTGAGTGGTTCAGCGGTGACAGCC 4973
|||||
1185 TGATAATCTCATGACCAAAATCCCTTAAACGAGTTTTCCTGAGTGGTTCAGCGGTGACAGCC 1126
|||||
4974 CGTAGAAGATCAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAAATCTGCTGCTT 5033
|||||

1125 CGTAGAAGATCAAGGATCTTCTTGAGATCCTTTTCTGCGGTAAATCTGCTGCTT 1066
|||||
5034 GCAAAACAAAAACACACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAAC 5093
|||||
1065 GCAAAACAAAAACACACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAAC 1006
|||||
5094 TCTTTTTCGGAAGGTAACTGGCTTCAGCAGAGCGAGATACCAATATCTGCTCTTACT 5153
|||||
1005 TCTTTTTCGGAAGGTAACTGGCTTCAGCAGAGCGAGATACCAATATCTGCTCTTACT 946
|||||
5154 GTAGCGGTAGTTAGGCGACCACTTCAAGAACTCTGTAGCAGCGCTACATATCTGCTCT 5213
|||||
945 GTAGCGGTAGTTAGGCGACCACTTCAAGAACTCTGTAGCAGCGCTACATATCTGCTCT 886
|||||
5214 GCTAATCTGTTTACAGTGGCTGCTCCAGTGGCGATTAAGTCTGTTTACCGGGTTGA 5273
|||||
885 GCTAATCTGTTTACAGTGGCTGCTCCAGTGGCGATTAAGTCTGTTTACCGGGTTGA 826
|||||
5274 CTCAGACGATAGTTTACCGGATTAAGCGCGAGCGGTGCGGCTGAAACGGGGGTTCTGCAC 5333
|||||
825 CTCAGACGATAGTTTACCGGATTAAGCGCGAGCGGTGCGGCTGAAACGGGGGTTCTGCAC 766
|||||
5334 ACAGCCAGCTTGGAGCGAAGCGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATG 5393
|||||
765 ACAGCCAGCTTGGAGCGAAGCGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATG 706
|||||
5394 AGAAGCGCCACGCTTCCGGAAGGAGGAGGAGCGGACAGGTATCCGGTAAAGCGGCAAGGT 5453
|||||
705 AGAAGCGCCACGCTTCCGGAAGGAGGAGGAGCGGACAGGTATCCGGTAAAGCGGCAAGGT 646
|||||
5454 CGGAACAGAGAGCGCAAGGAGCTTCCAGGGGAGGAAACGCTGATCTTTTATAGTCC 5513
|||||
645 CGGAACAGAGAGCGCAAGGAGCTTCCAGGGGAGGAAACGCTGATCTTTTATAGTCC 586
|||||
5514 TGTGCGGTTTCGCACTCTGACTTGGAGCGTGAATTTTGTGATGCTCGTCAGGGGGCG 5573
|||||
585 TGTGCGGTTTCGCACTCTGACTTGGAGCGTGAATTTTGTGATGCTCGTCAGGGGGCG 526
|||||
5574 GAGCCTATGAAAAACCGCAACCGCGCTTTTACGGTTTCTGCGCTTTTGTGCGC 5633
|||||
525 GAGCCTATGAAAAACCGCAACCGCGCTTTTACGGTTTCTGCGCTTTTGTGCGC 466
|||||
5634 TTTTGTCTCAGTCTTCTTCTGCGTTTACCGCTGATTTCTGCGATTAACCGTATTTACCG 5693
|||||
465 TTTTGTCTCAGTCTTCTTCTGCGTTTACCGCTGATTTCTGCGATTAACCGTATTTACCG 406
|||||
5694 CTTTGTAGTGTGATGATGCTGCGCGCAGCGCAACGACCGAGCGCAGTCAAGTGAAG 5753
|||||
405 CTTTGTAGTGTGATGATGCTGCGCGCAGCGCAACGACCGAGCGCAGTCAAGTGAAG 346
|||||
5754 CGAGAAACGGAAGAGCGCCCAATACGCAAAACCGCTTCTCCCGCGGTTGCGCGATCA 5813
|||||
345 CGAGAAACGGAAGAGCGCCCAATACGCAAAACCGCTTCTCCCGCGGTTGCGCGATCA 286
|||||
5814 TTAATGAG 5822
|||||
285 TTAATGAG 277
|||||

RESULT 5

AAD50589/C

ID AAD50589 standard; DNA; 3448 BP.

XX

AC AAD50589;

XX

DT 24-MAR-2003 (first entry)

XX

DE pGEMTElsh6 vector DNA.

XX

KW Hepatitis C virus; HCV; envelope protein; virucide; immunostimulant;

KW immune response; T-cell; therapy; infection; pharmaceutical; vaccine;

KW gene; da.

Qy	4674	TGAGCGTGGGTCTCGCGGTATCATATTGACGACTCTGGGCGAGATGGTAAAGCCCTCCCGGTAT	4733
Db	1425	TGAGCGTGGGTCTCGCGGTATCATATTGACGACACTGGGCGCAGATGGTAAAGCCCTCCCGGTAT	1366
Qy	4734	CGTAGTTATCTACACGACGGGGAGTCAAGCAACTATGGATGAACGAATATAGACAGATCGC	4793
Db	1365	CGTAGTTATCTACACGACGGGGAGTCAAGCAACTATGGATGAACGAATATAGACAGATCGC	1306
Qy	4794	TGAGATAGTGCCTCAGCTCATGTATTAAGCAATGGTAACTGTTCAGACCAGTTTACTCATATAT	4853
Db	1305	TGAGATAGTGCCTCAGCTCATGTATTAAGCAATGGTAACTGTTCAGACCAGTTTACTCATATAT	1246
Qy	4854	ACTTTAGATTGATTTAAACCTCAFTTTTAAATTTAAAGGATCTAGGTGAAGATTCCTTTT	4913
Db	1245	ACTTTAGATTGATTTAAACCTCAFTTTTAAATTTAAAGGATCTAGGTGAAGATTCCTTTT	1186
Qy	4914	TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGGGTCAGACCC	4973
Db	1185	TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGGGTCAGACCC	1126
Qy	4974	CGTAGAAAAGATCAAAAGATCTTCTTGAGATCTCTTTTTCGCGCGGTAACTCTGCTGCTT	5033
Db	1125	CGTAGAAAAGATCAAAAGATCTTCTTGAGATCTCTTTTTCGCGCGGTAACTCTGCTGCTT	1066
Qy	5034	GCAAAACAAAACCAACCGCTACACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAAC	5093
Db	1065	GCAAAACAAAACCAACCGCTACACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAAC	1006
Qy	5094	TCTTTTTCCGAAGGTAACTGGCTTCAGGAGAGCCAGATACCAAAATCTGCTCTTAGT	5153
Db	1005	TCTTTTTCCGAAGGTAACTGGCTTCAGGAGAGCCAGATACCAAAATCTGCTCTCTTAGT	946
Qy	5154	GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT	5213
Db	945	GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT	886
Qy	5214	GCTAATCCTGTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGGTGGA	5273
Db	885	GCTAATCCTGTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGGTGGA	826
Qy	5274	CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAAACGGGGGGTTCTGTCAC	5333
Db	825	CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAAACGGGGGGTTCTGTCAC	766
Qy	5334	ACGCCACGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGCAGCTATG	5393
Db	765	ACGCCACGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGCAGCTATG	706
Qy	5394	AGAAAGCGCCACGCTTCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAAGCGCAGGGT	5453
Db	705	AGAAAGCGCCACGCTTCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAAGCGCAGGGT	646
Qy	5454	CGGAACAGGAGAGCGCAGGAGAGCTTCAAGGGGGAAAACGCTTGGTATCTTTATAGTCC	5513
Db	645	CGGAACAGGAGAGCGCAGGAGAGCTTCAAGGGGGAAAACGCTTGGTATCTTTATAGTCC	586
Qy	5514	TGTCGGGTTTCGCCACCTCTGACTTTCGAGTTCGATTTTGTGATGCTCGTTCAGGGGGCG	5573
Db	585	TGTCGGGTTTCGCCACCTCTGACTTTCGAGTTCGATTTTGTGATGCTCGTTCAGGGGGCG	526
Qy	5574	GAGCCTATGGA AAAACGCCAGCAACGCGGCTTTTTCAGGTTCCTCGCTCTTTTCTGGCC	5633
Db	525	GAGCCTATGGA AAAACGCCAGCAACGCGGCTTTTTCAGGTTCCTCGCTCTTTTCTGGCC	466
Qy	5634	TTTTGCTCAGATGTTCTTTTCTGCGTTATCCCTGATCTGTGATTAACCGTATTTACCGC	5693
Db	465	TTTTGCTCAGATGTTCTTTTCTGCGTTATCCCTGATCTGTGATTAACCGTATTTACCGC	406
Qy	5694	CTTTGAGTGAGCTGATACCGCTCGCCGACCGCAACGACCGAGCGAGCGAGTCAGTGAG	5753
Db	405	CTTTGAGTGAGCTGATACCGCTCGCCGACCGCAACGACCGAGCGAGCGAGTCAGTGAG	346
Qy	5754	CGAGGAAGCGGAAGAGCGCCCAATACGCAAAACCGCTCTCTCCCGCGGTTTGGCGCGATTCA	5813

Db 645 CGGACAGGAGCGCAGCAGGAGCTTCAGGGGAAAAGCCCTGCTATCTTTATAGTCC 586
Qy 5514 TGTGCGGTTCGCCACCTCTGACTGAGCGTCGATTTTGTGATGCTGTCAGGGGGCG 5573
Db 585 TGTGCGGTTCGCCACCTCTGACTGAGCGTCGATTTTGTGATGCTGTCAGGGGGCG 526
Qy 5574 GAGCCTATGAAAAAGCCAGCAAGCGGCGCTTTTACGGTTCTGCGCTTTTGTGCGCC 5633
Db 525 GAGCCTATGAAAAAGCCAGCAAGCGGCGCTTTTACGGTTCTGCGCTTTTGTGCGCC 466
Qy 5634 TTTTGTCTCAGATGTTCTTCTGCTGATATCCCTGATTTCTGTGATTAACCGTATTACCGC 5693
Db 465 TTTTGTCTCAGATGTTCTTCTGCTGATATCCCTGATTTCTGTGATTAACCGTATTACCGC 406
Qy 5694 CTTTGTGAGTCAATACCGCTCCCGCAGCGAAGCAGCGAGCGAGTCAAGTGAG 5753
Db 405 CTTTGTGAGTCAATACCGCTCCCGCAGCGAAGCAGCGAGCGAGTCAAGTGAG 346
Qy 5754 CGAGGAGCGGAGAGCGCCCAATACCAACCGCTCTCCCGCGGTGGCGGATTCA 5813
Db 345 CGAGGAGCGGAGAGCGCCCAATACCAACCGCTCTCCCGCGGTGGCGGATTCA 286
Qy 5814 TTAATGCAG 5822
Db 285 TTAATGCAG 277

RESULT 7
AAX29905/c
ID AAX29905 standard; DNA; 3018 BP.
XX
AC AAX29905;
XX
DT 06-JUL-1999 (first entry)
XX
DE Plasmid pGEM (RTM)-T Easy Vector.
XX
KW Oligonucleotide; hybridisation; amidated polypeptide; hormone; primer;
XX amplification; rat; brain; cholecystokinin; CCK; amidation; hormone;
XX neurohormone; physiological role; plasmid; ss.
XX
OS Synthetic.
XX
PN W09910361-A1.
XX
PD 04-MAR-1999.
XX
PF 07-AUG-1998; 98WO-FR001767.
XX
PR 26-AUG-1997; 97FR-00010643.
XX
PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX
PI Martinez J, Goze C;
XX
DR WPI; 1999-204645/17.
XX
PT Oligonucleotides that hybridize to mRNA encoding precursors of amidated
PT hormones - useful for isolating new hormones.
XX
PS Disclosure; Page 19-21; 27pp; French.
XX
CC The invention relates to single-stranded oligonucleotides of 9-42
CC nucleotides that hybridize, under stringent or non-stringent conditions,
CC with mRNA encoding precursors of amidated polypeptide hormones. This
CC sequence represents the plasmid pGEM (RTM)-T Easy vector used to subclone
CC fragments of amidated polypeptide hormone coding sequences. The
CC oligonucleotides are used to identify new amidated polypeptide hormones
CC by hybridisation to cDNA encoding their precursors. cDNA encoding the
CC hormones, particularly neurohormones, can be expressed in microorganisms
CC and used therapeutically or to study their physiological roles
XX
SQ Sequence 3018 BP; 774 A; 747 C; 767 G; 730 T; 0 U; 0 Other;

Query Match 46.0%; Score 2675.4; DB 2; Length 3018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2676; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3146 TATAGTCAGTCGTATTAACAATTCTACCTGCGCGCTGTTTACCAACGTCGTGACCTGGGAAAC 3205
Db 3018 TATAGTCAGTCGTATTAACAATTCTACCTGCGCGCTGTTTACCAACGTCGTGACCTGGGAAAC 2959
Qy 3206 CTTGCGGCTTACCAACTTAATGCGCTTTCAGCAGCATCCCTTTTCGCCAGCTGGCGTAAAT 3265
Db 2958 CTTGCGGCTTACCAACTTAATGCGCTTTCAGCAGCATCCCTTTTCGCCAGCTGGCGTAAAT 2899
Qy 3266 AGCGAAGAGGCGCGCAGATCGGCTTCCCAACGTTGCGCAGCTGAATGGCGAATGG 3325
Db 2898 AGCGAAGAGGCGCGCAGATCGGCTTCCCAACGTTGCGCAGCTGAATGGCGAATGG 2839
Qy 3326 ACGGCGCTCTGAGCGGCGCATTAAGCGGCGGGTGTGTTGTTACGCGCAGCGTGACCG 3385
Db 2838 ACGGCGCTCTGAGCGGCGCATTAAGCGGCGGGTGTGTTGTTACGCGCAGCGTGACCG 2779
Qy 3386 CTACACTTGGCAGCGCCTAGCGCCGCTCTTTCGCTTTCTTCCCTTCTTTCGCGCA 3445
Db 2778 CTACACTTGGCAGCGCCTAGCGCCGCTCTTTCGCTTTCTTCCCTTCTTTCGCGCA 2719
Qy 3446 CGTTGCGCGGCTTTCGCCGCTCAAGCTCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTA 3505
Db 2718 CGTTGCGCGGCTTTCGCCGCTCAAGCTCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTA 2659
Qy 3506 GAGCTTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATGTTTCACTAGTGGGC 3565
Db 2658 GAGCTTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATGTTTCACTAGTGGGC 2599
Qy 3566 CATCGCCCTGATAGACGGTTTTCGCCCTTTGAGCTTGGAGTCCACAGTTCTTTAATAGTG 3625
Db 2598 CATCGCCCTGATAGACGGTTTTCGCCCTTTGAGCTTGGAGTCCACAGTTCTTTAATAGTG 2539
Qy 3626 GACTCTTGTTCAAAACCTGGAACAAACATCAACCCCTATCTCGGCTATTTCTTTGATTTAT 3685
Db 2538 GACTCTTGTTCAAAACCTGGAACAAACATCAACCCCTATCTCGGCTATTTCTTTGATTTAT 2479
Qy 3686 AAGGGATTTTGGCGATTTTCGSCCTATTGTTTAAAAAATGAGCTGATTTTAAACAAATTTTA 3745
Db 2478 AAGGGATTTTGGCGATTTTCGSCCTATTGTTTAAAAAATGAGCTGATTTTAAACAAATTTTA 2419
Qy 3746 ACAGCAATTTTAAACAAATATTAAAGCTTTTACAAATTCGCCCTGATGCGGTATTTCTCCTT 3805
Db 2418 ACAGCAATTTTAAACAAATATTAAAGCTTTTACAAATTTTCGCCCTGATGCGGTATTTCTCCTT 2359
Qy 3806 ACAGCTCTGCGGTATTTTCACCGCATACAGGTGGCATTTTTCGGGGAAATGTGCGCG 3865
Db 2358 ACAGCTCTGCGGTATTTTCACCGCATACAGGTGGCATTTTTCGGGGAAATGTGCGCG 2299
Qy 3866 GAACCCCTATTGTTTATTTTCTTAATACATCAAAATATGATATCCGCTCATGAGACAAT 3925
Db 2298 GAACCCCTATTGTTTATTTTCTTAATACATCAAAATATGATATCCGCTCATGAGACAAT 2239
Qy 3926 AACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGATGAGTATTTCAACATTTCC 3985
Db 2238 AACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGATGAGTATTTCAACATTTCC 2179
Qy 3986 GTGTGCGCCCTTATTCCTTTTTCGGCATTTTTCGCTTCTGTTTTCCTCACCAGAAA 4045
Db 2178 GTGTGCGCCCTTATTCCTTTTTCGGCATTTTTCGCTTCTGTTTTCCTCACCAGAAA 2119
Qy 4046 CGCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAACAGTGGTTTACATCGAAC 4105
Db 2118 CGCTGCTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCAACAGTGGTTTACATCGAAC 2059
Qy 4106 TGGATCTCAACAGCGGTAAAGATCTTCAGAGTCTTTCGCCCCCGAAGAGAGCTTTTCCAAATGA 4165
Db 2058 TGGATCTCAACAGCGGTAAAGATCTTCAGAGTCTTTCGCCCCCGAAGAGAGCTTTTCCAAATGA 1999

QY 4166 TGAGCACTTTTAAAGTTCTGCTATGTGGCCGGGTATATATCCCGTATTTAGCGCGGGCAAG 4225
DB 1998 TGAGCACTTTTAAAGTTCTGCTATGTGGCCGGGTATATATCCCGTATTTAGCGCGGGCAAG 1939
QY 4226 AGCAACTCGGTCCCGCATACACTATTCTCAGAAATGACTTGGTTAGTACTCACCAAGTCA 4285
DB 1938 AGCAACTCGGTCCCGCATACACTATTCTCAGAAATGACTTGGTTAGTACTCACCAAGTCA 1879
QY 4286 CAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATTTATGCAAGTGTGCCATAACCA 4345
DB 1878 CAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATTTATGCAAGTGTGCCATAACCA 1819
QY 4346 TGAGTATTAACACTGCGGCCCAACTTACTTCTGACACAGATCGAGAGACCGAAGAGCTAA 4405
DB 1818 TGAGTATTAACACTGCGGCCCAACTTACTTCTGACACAGATCGAGAGACCGAAGAGCTAA 1759
QY 4406 CCGCTTTTGGCAACAATCGGGGATCATGTAACTGCGCTTGTGATGCTGTGGAAACCGGAGC 4465
DB 1758 CCGCTTTTGGCAACAATCGGGGATCATGTAACTGCGCTTGTGATGCTGTGGAAACCGGAGC 1599
QY 4466 TGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCGCTGTAGCAATGCCAACAA 4525
DB 1698 TGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCGCTGTAGCAATGCCAACAA 1639
QY 4526 CGTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAG 4585
DB 1638 CGTTGGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAG 1579
QY 4586 ACTGGATGAGGCGGATTAAGTTGCGAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCT 4645
DB 1578 ACTGGATGAGGCGGATTAAGTTGCGAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCT 1519
QY 4646 GGTATTATGCTGATAAATCTGAGCGCGGTGAGCGTGCGTCTCGCGGTATCATTTGCGACAC 4705
DB 1518 GGTATTATGCTGATAAATCTGAGCGCGGTGAGCGTGCGTCTCGCGGTATCATTTGCGACAC 1459
QY 4706 TGGGGCCAGATGTTAGCCCTCCCGTATCGTAGTTATCTACAGACGCGGAGTCAAGCAAA 4765
DB 1458 TGGGGCCAGATGTTAGCCCTCCCGTATCGTAGTTATCTACAGACGCGGAGTCAAGCAAA 1399
QY 4766 CTATGATGAACGAATAGACAGATCGCTGAGTAGTGTCTCAGTATGATTAAGCATTTGT 4825
DB 1398 CTATGATGAACGAATAGACAGATCGCTGAGTAGTGTCTCAGTATGATTAAGCATTTGT 1339
QY 4826 AACTGTGACACCAAGTTTACTCATATATCTTTAGATTTGATTTAAAACTTCATTTTAAAT 4885
DB 1338 AACTGTGACACCAAGTTTACTCATATATCTTTAGATTTGATTTAAAACTTCATTTTAAAT 1279
QY 4886 TTAAGGATCTAGGTGAAGATCGTTTGTGATATCTCATGACCAAAATCCCTTAAGCTG 4945
DB 1278 TTAAGGATCTAGGTGAAGATCGTTTGTGATATCTCATGACCAAAATCCCTTAAGCTG 1219
QY 4946 AGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGATCTTCTTGAGATC 5005
DB 1218 AGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAGATCTTCTTGAGATC 1159
QY 5006 CTTTTTTTTCGCGGTAAATCTGCTGTTGCAAAACAAAACCAACCCCTACCGCGGTGG 5065
DB 1158 CTTTTTTTTCGCGGTAAATCTGCTGTTGCAAAACAAAACCAACCCCTACCGCGGTGG 1099
QY 5066 TTTTGTGTCGGGATCAAGAGTACCAACTCTTTTTCGAGAGTAACTGGCTTCAGCAGAG 5125
DB 1098 TTTTGTGTCGGGATCAAGAGTACCAACTCTTTTTCGAGAGTAACTGGCTTCAGCAGAG 1039
QY 5126 CGCAGATACCAAAATCTGCTCTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACT 5185
DB 1038 CGCAGATACCAAAATCTGCTCTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACT 979
QY 5186 CTGTAGCACCGCTTACATACCTCGCTCTGCTTAATCTGTTACCAAGTGGCTGCTGCCAGTG 5245
DB 978 CTGTAGCACCGCTTACATACCTCGCTCTGCTTAATCTGTTACCAAGTGGCTGCTGCCAGTG 919
QY 5246 GCGATAAGTCTGCTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGC 5305

DB 918 GCGATAAGTCTGCTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGC 859
QY 5306 GGTTCGGCTGCAACGCGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAAACGACCTTACACCG 5365
DB 858 GGTTCGGCTGCAACGCGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAAACGACCTTACACCG 799
QY 5366 AACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGGAAGG 5425
DB 798 AACTGAGATACCTACAGCGGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGGAAGG 739
QY 5426 CGACACAGATACCGGTAAAGCGGCGAGGTCGGAACAGAGAGCGCACGAGGAGCTTCCAG 5485
DB 738 CGACACAGATACCGGTAAAGCGGCGAGGTCGGAACAGAGAGCGCACGAGGAGCTTCCAG 679
QY 5486 GGGGAAACGCTGCTGATCTTTATAGTCTGTGCGGTTTCGCCACTCTGTACTTCAGCGCTC 5545
DB 678 GGGGAAACGCTGCTGATCTTTATAGTCTGTGCGGTTTCGCCACTCTGTACTTCAGCGCTC 619
QY 5546 GATTTTGTGATCTGCTCAGGGGGCGGAGCGCTATGGAATAAGCGCAAGCGGCGCT 5605
DB 618 GATTTTGTGATCTGCTCAGGGGGCGGAGCGCTATGGAATAAGCGCAAGCGGCGCT 559
QY 5606 TTTTACGTTCTGCGCTTTGCTGCGCTTTTGTCTACATGTTCTTCTCGCTGCTATCCC 5665
DB 558 TTTTACGTTCTGCGCTTTTGTCTGCGCTTTTGTCTACATGTTCTTCTCGCTGCTATCCC 499
QY 5666 CTGATCTCTGTGATAACCGCTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCAGCC 5725
DB 498 CTGATCTCTGTGATAACCGCTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCAGCC 439
QY 5726 GAACGACCGAGCGCAGCTGAGTGAGCGAGGAGCGAGAGCGGCGCCCAATACGCAAAC 5785
DB 438 GAACGACCGAGCGCAGCTGAGTGAGCGAGGAGCGAGAGCGGCGCCCAATACGCAAAC 379
QY 5786 CGCTCTCCCGCGCTGCGCGGATTCATTAAATGCGAG 5822
DB 378 CGCTCTCCCGCGCTGCGCGGATTCATTAAATGCGAG 342

RESULT 8
AAD0980/c
ID AAD0980 standard; DNA; 5919 BP.
XX
AC AAD0980;
XX AC
DT 12-SBP-2001 (first entry)
XX
DB phSP-GUS construct for transfection of pacific oysters.
XX
KW Fruitfly; fertility; reproduction; gametogenesis; microinjection; GUS;
KW glucuronidase; infection; plasmid phSP-GUS; HSP; heat shock promoter;
KW embryogenesis; ds.
XX
OS Drosophila melanogaster.
OS Unidentified.
OS Chimeric.
XX
PN WO200148224-A1.
XX
PD 05-JUL-2001.
XX
PP 22-DEC-2000; 2000WO-AU001596.
XX
PR 24-DEC-1999; 99AU-00004884.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Thresher R, Hinds L, Hardy C, Whyard S, Vignarajan S, Grewe PM;
PI Patil J;
XX
DR WPI; 2001-425672/45.
XX

Db 2748 GCGGGTGTGGTTCACGCGAGGTCACGCTACACTTGCAGCGCCCTAGCGCCCGC 2689
Qy 3414 TCCTTTCCGCTTTCTTCCCTCTCCCTTCTCGCCACAGTTCCGCGCTTTTCCCGTCAAGCTCT 3473
Db 2688 TCCTTTCCGCTTTCTTCCCTCTCCCTTCTCGCCACAGTTCCGCGCTTTTCCCGTCAAGCTCT 2629
Qy 3474 AAATCGGGGGTCCCTTTAGGGTTCGGAATTTAGAGCTTTACGGCACTTCGACCGCAAAAA 3533
Db 2628 AAATCGGGGGTCCCTTTAGGGTTCGGAATTTAGAGCTTTTACGGCACTTCGACCGCAAAAA 2569
Qy 3534 ACTTGATTTGGGTGATGCTTCACGTPAGTGGCCATCGCCCTGATAGAGCGTTTTCGCCC 3593
Db 2568 ACTTGATTTAGGGTATGCTTCACGTPAGTGGCCATCGCCCTGATAGAGCGTTTTCGCCC 2509
Qy 3594 TTTGACGTTGGAGTCCAGTTCTTTAAATAGTGGACTCTTTGTTCCAAACTGGAAACAACACT 3653
Db 2508 TTTGAGGTTGGAGTCCAGTTCTTTAAATAGTGGACTCTTTGTTCCAAACTGGAAACAACACT 2449
Qy 3654 CAACCTATCTCGGCTATCTTTTGAATTTAAGGGATTTTGGCGATTTGCGGCTATTG 3713
Db 2448 CAACCTATCTCGGCTATCTTTTGAATTTAAGGGATTTTGGCGATTTGCGGCTATTG 2389
Qy 3714 GTTAAATAATGAGCTGATTTTAAACAATATTTAACCGGAATTTTAAACAATATTTAAAGCT 3773
Db 2388 GTTAAATAATGAGCTGATTTTAAACAATATTTAACCGGAATTTTAAACAATATTTAAAGCT 2329
Qy 3774 TACAAATTTCCGCTGATCGGCTATTTTCTCTTACGCACTCTGTCGCTATTTTACACCGCA 3833
Db 2328 TACAAATTT - CCTGATCGGCTATTTTCTCTTACGCACTCTGTCGCTATTTTACACCGCA 2271
Qy 3834 TACAGTGGCACTTTTCCGGGAAATGTGGCGGAAACCCCTATTTGTTTATTTTCTAAAT 3893
Db 2270 T - CAGTGGCACTTTTCCGGGAAATGTGGCGGAAACCCCTATTTGTTTATTTTCTAAAT 2212
Qy 3894 ACATTTCAATATGATCGCTCATCAGACAAATACCTGATAAATGCTTCAATATATG 3953
Db 2152 ACATTTCAATATGATCGCTCATCAGACAAATACCTGATAAATGCTTCAATATATG 2152
Qy 3954 AAAAGGAAGATGATGATTTCAACATTTTCGCTGTCGCCCTTATTTCCCTTTTTCGCGC 4013
Db 2151 AAAAGGAAGATGATGATTTCAACATTTTCGCTGTCGCCCTTATTTCCCTTTTTCGCGC 2092
Qy 4014 ATTTTGCCTTCTGTTTTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 4073
Db 2091 ATTTTGCCTTCTGTTTTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 2032
Qy 4074 TCAGTTGGGTGACAGTGGGTTACATCGAATGATGAGCACTTTTAAAGTTCTGCTATGTTG 4133
Db 2031 TCAGTTGGGTGACAGTGGGTTACATCGAATGATGAGCACTTTTAAAGTTCTGCTATGTTG 1972
Qy 4134 GAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTTG 4193
Db 1971 GAGTTTTCGCCCGGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTTG 1912
Qy 4194 CGGGTATTTATCCGTTATGACGCGCGGCAAGAGCAATCGGTTCGCGCATACACTATTC 4253
Db 1911 CGGGTATTTATCCGTTATGACGCGCGGCAAGAGCAATCGGTTCGCGCATACACTATTC 1852
Qy 4254 TCAGATGATGTTGGTTGATGATCTACACAGTTCACAGAAAGCATCTTACGGATGGCATTC 4313
Db 1851 TCAGATGATGTTGGTTGATGATCTACACAGTTCACAGAAAGCATCTTACGGATGGCATTC 1792
Qy 4314 AGTAAGAGAAATATGCACTGCTGCCATACCATGATGATTAACACTGCGGCCAACTTACT 4373
Db 1791 AGTAAGAGAAATATGCACTGCTGCCATTAACCATGATGATTAACACTGCGGCCAACTTACT 1732
Qy 4374 TCTGACAAACGATCGAGGACCGAAGAGCTAACCGCTTTTTCGACAAACATGCGGGATCA 4433
Db 1731 TCTGACAAACGATCGAGGACCGAAGAGCTAACCGCTTTTTCGACAAACATGCGGGATCA 1672
Qy 4434 TGTAACTCGCTTGTATCTTGGGACCGGAGCTGAATGAACCAATACCAACGACGAGG 4493

Db 1671 TGTAACTCGCTTGTATCTTGGGACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 1612
Qy 4494 TGACACCAACGATGCTGTAGCAATGGCAACAACTGTTGCGCAAACTATTAACTGGCGAACT 4553
Db 1611 TGACACCAACGATGCTGTAGCAATGGCAACAACTGTTGCGCAAACTATTAACTGGCGAACT 1552
Qy 4554 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGGAGGGGATTAAGTTTCAGG 4613
Db 1551 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGGAGGGGATTAAGTTTCAGG 1492
Qy 4614 ACCACTTCTCGCTCGCGCCCTTCCGCTGCTGTTTAAATGCTGATTAATCTGGAGCCGG 4673
Db 1491 ACCACTTCTCGCTCGCGCCCTTCCGCTGCTGTTTAAATGCTGATTAATCTGGAGCCGG 1432
Qy 4674 TGAGCGTGGTCTCGCGCTATCATTTGACGACTGCGGCGCAGATGTTAAGCCTCCCGTAT 4733
Db 1431 TGAGCGTGGTCTCGCGCTATCATTTGACGACTGCGGCGCAGATGTTAAGCCTCCCGTAT 1372
Qy 4734 GGTAGTTATCTACAGGACGGGGAGTCAGCAACTATGATGAAACGAAATAGACAGATCCG 4793
Db 1371 GGTAGTTATCTACAGGACGGGGAGTCAGCAACTATGATGAAACGAAATAGACAGATCCG 1312
Qy 4794 TGAGATAGTCTCTCACTGATTTAAGCAATTTGTTAACTGTCAGACCAAGTTTACTCATATAT 4853
Db 1311 TGAGATAGTCTCTCACTGATTTAAGCAATTTGTTAACTGTCAGACCAAGTTTACTCATATAT 1252
Qy 4854 ACTTTAGATTTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTT 4913
Db 1251 ACTTTAGATTTGATTTAAACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTT 1192
Qy 4914 TGATATCTCATGACCAAAATCCCTTAACTGAGATTTTCTGTTCCACTGAGCGTCAGACCC 4973
Db 1191 TGATATCTCATGACCAAAATCCCTTAACTGAGATTTTCTGTTCCACTGAGCGTCAGACCC 1132
Qy 4974 CGTAGAAAGATCAAGGATCTTCTTGAGATCTTTTCTGCGGCTAATCTGCTGCTT 5033
Db 1131 CGTAGAAAGATCAAGGATCTTCTTGAGATCTTTTCTGCGGCTAATCTGCTGCTT 1072
Qy 5034 GCAACAAACAAACACACCGCTACACGCGTGGTGTGTTGTCGCGGATCAAGAGTACCAAC 5093
Db 1071 GCAACAAACAAACACACCGCTACACGCGTGGTGTGTTGTCGCGGATCAAGAGTACCAAC 1012
Qy 5094 TCTTTTTCGAGGTAACTGGCTTCAGCAGAGCGCAGATACCAATACCTGCTCTCTAGT 5153
Db 1011 TCTTTTTCGAGGTAACTGGCTTCAGCAGAGCGCAGATACCAATACCTGCTCTCTAGT 952
Qy 5154 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 5213
Db 951 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 892
Qy 5214 GCTAATCTGTTACAGTGGCTGCTGCGAGTGAATAGTGTGCTTTTACCGGGTTGGA 5273
Db 891 GCTAATCTGTTACAGTGGCTGCTGCGAGTGAATAGTGTGCTTTTACCGGGTTGGA 832
Qy 5274 CTCAGACGATGATTACCGGATNAGCGCGGCTGGGCTGAACGGGGGTTCTGTCAC 5333
Db 831 CTCAGACGATGATTACCGGATNAGCGCGGCTGGGCTGAACGGGGGTTCTGTCAC 772
Qy 5334 ACAGCCAGCTTTGAGCGCAACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATG 5393
Db 771 ACAGCCAGCTTTGAGCGCAACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATG 712
Qy 5394 AGAAGCGCCACGCTTCCGGAAGGGAGAAAGCGGACAGGTTATCCGGTAAAGCGGAGGT 5453
Db 711 AGAAGCGCCACGCTTCCGGAAGGGAGAAAGCGGACAGGTTATCCGGTAAAGCGGAGGT 652
Qy 5454 CGGACAGGAGCGCAGGAGCTTCCAGGGGGAACCGCTGCTATCTTTTAGTCC 5513
Db 651 CGGACAGGAGCGCAGGAGCTTCCAGGGGGAACCGCTGCTATCTTTTAGTCC 592
Qy 5514 TGTGGGTTTCCCACTCTGACTTGAAGCTCGATTTTGTGATGCTCGTAGGGGGGGG 5573
Db 591 TGTGGGTTTCCCACTCTGACTTGAAGCTCGATTTTGTGATGCTCGTAGGGGGGGG 532

QY 5574 GAGCCTATGAAAAACCCAGCAACCGCGGCTTTTACGGTTCCTGCGCTTTTCTGCTGGCC 5633
DB 531 GAGCCTATGAAAAACCCAGCAACCGCGGCTTTTACGGTTCCTGCGCTTTTCTGCTGGCC 472
QY 5634 TTTTGTCTCACAATGTTCTTCTGCTGTTATCCCTGATTTCTGTGATAAACCGTATTACCGC 5693
DB 471 TTTTGTCTCACAATGTTCTTCTGCTGTTATCCCTGATTTCTGTGATAAACCGTATTACCGC 412
QY 5694 CTTTGTAGTGAGCTGATACCGCTCGCGCAGCCGCAACGACCGAGCGAGCGAGTCAGTGAG 5753
DB 411 CTTTGTAGTGAGCTGATACCGCTCGCGCAGCCGCAACGACCGAGCGAGTCAGTGAG 352
QY 5754 CGAGGAGCGAGAGCGCCCAATACGCAACCGCTCTCCCGCGGCTTGGCGGATTC 5813
DB 351 CGAGGAGCGAGAGCGCCCAATACGCAACCGCTCTCCCGCGGCTTGGCGGATTC 292
QY 5814 TTAATGCGAG 5822
DB 291 TTAATGCGAG 283

RESULT 10

ABT16597/c

ID ABT16597 standard; DNA; 3357 BP.

XX ABT16597;

DT 03-APR-2003 (first entry)

XX Artificial plant chromosome related plasmid DNA SEQ ID No 7.

DE Plant artificial chromosome; PAC; transgenic plant; vaccine;

KW blood factor; herbicide; stress; agronomical; nutrient quality;

KW bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;

KW ds.

XX Unidentified.

XX WO200296923-A1.

XX 05-DEC-2002.

XX 30-MAY-2002; 2002WO-US017451.

XX 30-MAY-2001; 2001US-0294687P.

PR 04-JUN-2001; 2001US-0296329P.

XX (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

PA (AGRI-) AGRISOMA INC.

XX Perez C, Fabijanski SF, Perkins E;

XX WPI; 2003-140436/13.

DR

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CC heterologous nucleic acid optionally encodes a product that provides an
CC agronomically important trait in the plant, e.g. a product that alters
CC nutrient use and/or improves the nutrient quality of the plant. The
CC heterologous nucleic acid is contained within a bacterial artificial
CC chromosome (BAC) or a yeast artificial chromosome (YAC). This
CC polynucleotide sequence represents the DNA of a plasmid used in the
CC method of the invention
XX
SQ Sequence 3357 BP; 854 A; 821 C; 851 G; 831 T; 0 U; 0 Other;

Query Match 45.9%; Score 2670.2; DB 7; Length 3357;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2698; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 3114 CGCCCGATGCGAGCTGCGGCCCAATTCGCCCTATAGTAGTGTATACAAATTCACGTG 3173
DB 2988 CGCGAGCATCGAGCTGCGGCCCAATTCGCCCTATAGTAGTGTATACAAATTCACGTG 2929
QY 3174 CGCTCGTTCACAACTGCTGACTGGGAAACCTCGCGTTCACCACTTAATCGCCTTG 3233
DB 2928 CGCTCGTTCACAACTGCTGACTGGGAAACCTCGCGTTCACCACTTAATCGCCTTG 2869
QY 3234 CAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT 3293
DB 2868 CAGCACATCCCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTT 2809
QY 3294 CCCAACAGTTGCGCAGCTGAATGGCGAATGAGCAGCCCTCTAGTAGCGGCGATTAAGGC 3353
DB 2808 CCCAACAGTTGCGCAGCTGAATGGCGAATGAGCAGCCCTCTAGTAGCGGCGATTAAGGC 2749
QY 3354 GCGGGTGTGGTGTACCGCGAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCCGC 3413
DB 2748 GCGGGTGTGGTGTACCGCGAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCCGC 2689
QY 3414 TCCTTTCGCTTTCTTCCCTTCTTCGCCAGCTTTCGCCGCTTTCGCCGCTCAAGCTCT 3473
DB 2688 TCCTTTCGCTTTCTTCCCTTCTTCGCCAGCTTTCGCCGCTTTCGCCGCTCAAGCTCT 2629
QY 3474 AAATCGGGGCTCCCTTTTAGGGTTCGATTTAGAGCTTTACGGCAGCTTCGACCGCAAAA 3533
DB 2628 AAATCGGGGCTCCCTTTTAGGGTTCGATTTAGAGCTTTACGGCAGCTTCGACCGCAAAA 2569
QY 3534 ACTTGATTTGGGTGATGTTTACGTAGTGGCCCATCGCCCTGATAGACGCTTTTCGCC 3593
DB 2568 ACTTGATTTGGGTGATGTTTACGTAGTGGCCCATCGCCCTGATAGACGCTTTTCGCC 2509
QY 3594 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCTCAAACTGGAACA 3653
DB 2508 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCTCAAACTGGAACA 2449
QY 3654 CAACCTATCTCGCTCTATTTCTTTGATTTAAGGGATTTTCGCCGATTTTCGCCCTATTG 3713
DB 2448 CAACCTATCTCGCTCTATTTCTTTGATTTAAGGGATTTTCGCCGATTTTCGCCCTATTG 2389
QY 3714 GTTAAAAATGAGCTGATTTTAAACAAATATTTAAACGCAATTTTAAACAAATATTA 3773
DB 2388 GTTAAAAATGAGCTGATTTTAAACAAATATTTAAACGCAATTTTAAACAAATATTA 2329
QY 3774 TACAAATTTTCGCCCTGATGCGGTATTTTCTCCTTACGCTCTGTGCGGTATTTCAACGCA 3833
DB 2328 TACAAATTTTTCGCCCTGATGCGGTATTTTCTCCTTACGCTCTGTGCGGTATTTCAACGCA 2271
QY 3834 TACAGTGGCAGCTTTTCGCCGAAATGTCGCCGAAACCCCTATTGTTTATTTTCTAAAT 3893
DB 2270 T-CAGTGGCAGCTTTTTCGCCGAAATGTCGCCGAAACCCCTATTGTTTATTTTCTAAAT 2212
QY 3894 ACATTCAAAATATGATTCCTCTCATGAGCAATAACCTCTGATAATGCTTCAATAATATG 3953
DB 2211 ACATTCAAAATATGATTCCTCTCATGAGCAATAACCTCTGATAATGCTTCAATAATATG 2152
QY 3954 AAAAAAGAGAGTAGTAGTATTCAACATTTTCGCTGTGCGCCCTATTTCCTTTTTCGGCG 4013
DB 2151 AAAAAAGAGAGTAGTAGTATTCAACATTTTCGCTGTGCGCCCTATTTCCTTTTTCGGCG 2092

QY 4014 ATTTTGGCTTCTGTTTTGCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 4073
DB 2091 ATTTTGGCTTCTGTTTTGCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 2032
QY 4074 TCAGTTGGGTGCAAGAGTGGGTATCATGCAACTGATGATCTCAACAGCGTAAAGTCTCTTGA 4133
DB 2031 TCAGTTGGGTGCAAGAGTGGGTATCATGCAACTGATGATCTCAACAGCGTAAAGTCTCTTGA 1972
QY 4134 GAGTTTTGCGCCGGAAGAAAGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCG 4193
DB 1971 GAGTTTTGCGCCGGAAGAAAGTTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCG 1912
QY 4194 CGCGTATTTATCCGTTATTTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATATTC 4253
DB 1911 CGCGTATTTATCCGTTATTTGACGCGGCAAGAGCAACTCGGTGCGCGCATACATATTC 1852
QY 4254 TCAGAAATGACTTGGTTGATGATCTCAACAGTCAAGAAAGCACTTTACGGATGCGATGAC 4313
DB 1851 TCAGAAATGACTTGGTTGATGATCTCAACAGTCAAGAAAGCACTTTACGGATGCGATGAC 1792
QY 4314 AGTAAGAGAAATTAAGCACTGCTGCTCAATACCACTGATGATTAACACTGCGGCAACTTACT 4373
DB 1791 AGTAAGAGAAATTAAGCACTGCTGCTCAATACCACTGATGATTAACACTGCGGCAACTTACT 1732
QY 4374 TCTGACAAACGATCGGAGGACCGAAGGAGCTAAACGCTTTTTTGGCAAAACATGGGGGATCA 4433
DB 1731 TCTGACAAACGATCGGAGGACCGAAGGAGCTAAACGCTTTTTTGGCAAAACATGGGGGATCA 1672
QY 4434 TGTAATCTGCTTGTGATCTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGGAGCG 4493
DB 1671 TGTAATCTGCTTGTGATCTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGGAGCG 1612
QY 4494 TGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACCTGGCGAACT 4553
DB 1611 TGACACCAAGATGCTGTAGCAATGGCAACACGTTGCGCAAACTATTAACCTGGCGAACT 1552
QY 4554 ACTTACTCTAGCTTCTCCGCGCAACAAATTAATAGACTGGATGGAGGCGGATAAAGTTGCGAG 4613
DB 1551 ACTTACTCTAGCTTCTCCGCGCAACAAATTAATAGACTGGATGGAGGCGGATAAAGTTGCGAG 1492
QY 4614 ACCACTTCTGCGCTCGGCGCTTCCGCTGGCTGGTTATTTGCTGATAAATCTGGAGCGG 4673
DB 1491 ACCACTTCTGCGCTCGGCGCTTCCGCTGGCTGGTTATTTGCTGATAAATCTGGAGCGG 1432
QY 4674 TGAGCTGGGTCTCGCGGTATCATTTGACGACTGGGCGCAGATGGTAAGCCCTCCCGTAT 4733
DB 1431 TGAGCTGGGTCTCGCGGTATCATTTGACGACTGGGCGCAGATGGTAAGCCCTCCCGTAT 1372
QY 4734 CGTATGTTATCTACAGCGGGAGTCAAGCAACTATGGATGAACGAATAGACGATCGC 4793
DB 1371 CGTATGTTATCTACAGCGGGAGTCAAGCAACTATGGATGAACGAATAGACGATCGC 1312
QY 4794 TGAGATAGGTGCTCCTCATGATTAAGCATTTGATGCTGACCAAGTTTACTCATATAT 4853
DB 1311 TGAGATAGGTGCTCCTCATGATTAAGCATTTGATGCTGACCAAGTTTACTCATATAT 1252
QY 4854 ACTTTAGATGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 4913
DB 1251 ACTTTAGATGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTT 1192
QY 4914 TGATAATCTCATGACCAAAATCCCTTAACGTTGTTTCCATGAGCGTCAAGCC 4973
DB 1191 TGATAATCTCATGACCAAAATCCCTTAACGTTGTTTCCATGAGCGTCAAGCC 1132
QY 4974 CGTAGAAAAGATCAAGAGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTT 5033
DB 1131 CGTAGAAAAGATCAAGAGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTT 1072
QY 5034 GCAACCAAAAGAACACCGCTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAAC 5093
DB 1071 GCAACCAAAAGAACACCGCTACAGCGGTGTTTGTGCGGATCAAGAGCTACCAAC 1012

QY 5094 TCTTTTTCGGAAGGTAACTGGCTTCAGCAGCGCAGATACCAAAATACATGTCCTTCTAGT 5153
DB 1011 TCTTTTTCGGAAGGTAACTGGCTTCAGCAGCGCAGATACCAAAATACATGTCCTTCTAGT 952
QY 5154 GTAGCGGTAGTTAGGCGCACCACTTCAAGNACTCTGTAGCACCGCCTACATACCTCGCTCT 5213
DB 951 GTAGCGGTAGTTAGGCGCACCACTTCAAGNACTCTGTAGCACCGCCTACATACCTCGCTCT 892
QY 5214 GCTAATCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAGTCTGTCTTTACCGGGTTGA 5273
DB 891 GCTAATCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAGTCTGTCTTTACCGGGTTGA 832
QY 5274 CTCAGACGATAGTTACCGGATAGCGGAGCGGTCGGCTCGAAACGCGGGGTTCTGTCAC 5333
DB 831 CTCAGACGATAGTTACCGGATAGCGGAGCGGTCGGCTCGAAACGCGGGGTTCTGTCAC 772
QY 5334 ACAGCCGAGCTTTGGAGCGAAGCGACCTACACGAACTGAGATACCTACAGCGTGAGCTATG 5393
DB 771 ACAGCCGAGCTTTGGAGCGAAGCGACCTACACGAACTGAGATACCTACAGCGTGAGCTATG 712
QY 5394 AGAAGCGCCACGCTTCCGAAGGAGGAAAGCGGACAGGTATCCGGTAAGCGGCAAGGT 5453
DB 711 AGAAGCGCCACGCTTCCGAAGGAGGAAAGCGGACAGGTATCCGGTAAGCGGCAAGGT 652
QY 5454 CGBAACAGGAGAGCGACGAGGAGCTTCCAGGGGAAACGCTCGTATCTTTATAGTCC 5513
DB 651 CGBAACAGGAGAGCGACGAGGAGCTTCCAGGGGAAACGCTCGTATCTTTATAGTCC 592
QY 5514 TGTGCGGTTTCCGCACTCTGACTTTGAGCGTCAATTTTGTGATGCTCGTCAGGGGGCG 5573
DB 591 TGTGCGGTTTCCGCACTCTGACTTTGAGCGTCAATTTTGTGATGCTCGTCAGGGGGCG 532
QY 5574 GAGCTATGGAAGAAACGCGACCAACGCGGCTTTTACGGTTCTGCGCTTTTGTGGCC 5633
DB 531 GAGCTATGGAAGAAACGCGACCAACGCGGCTTTTACGGTTCTGCGCTTTTGTGGCC 472
QY 5634 TTTTGTCTCAGATGTTTCTGCTGCTGATTTCCCTGATTTCTGTGATTAACCGTATTTACCG 5693
DB 471 TTTTGTCTCAGATGTTTCTGCTGCTGATTTCCCTGATTTCTGTGATTAACCGTATTTACCG 412
QY 5694 CTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGAGCGCAGCGAGTCAAGTGAAG 5753
DB 411 CTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGAGCGCAGCGAGTCAAGTGAAG 352
QY 5754 CGAGGAAGCGGAAGAGCGCCCAATACGCAAAACGCTCTCCCGCGGCTGTCGCGGATCA 5813
DB 351 CGAGGAAGCGGAAGAGCGCCCAATACGCAAAACGCTCTCCCGCGGCTGTCGCGGATCA 292
QY 5814 TTAATGCGAG 5822
DB 291 TTAATGCGAG 283

RESULT 11
ADA94775/c

ID ADA94775 standard; DNA; 4514 BP.

XX ADA94775;
ACXX 20-NOV-2003 (first entry)
DTXX Plasmid pGL2neo (+) #S8Q ID 4.
DEXX Lymphocyte; vertebrate; antibody; genetically modified; ds.
KWXX Synthetic.
OSXX EP1321477-A1.
FNXX 25-JUN-2003.
PDXX 22-DEC-2001; 2001EP-00130805.
PP

XX

SQ	Sequence	9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 0 U; 3 Other;
	Query Match	45.7%; Score 2658.4; DB 6; Length 9359;
	Best Local Similarity	99.7%; Pred. No. 0;
	Matches 2685; Conservative	0; Mismatches 6; Indels 3; Gaps 2;
QY	3129	TCGGGCCCAATTCGGCCCTATAGTACGTCGTATTACAAATTCACATTCGCGCGTGTGTTTAAAC 3188
DB	4	TCGGGCCCAATTCGGCCCTATAGTACGTCGTATTACAAATTCACATTCGCGCGTGTGTTTAAAC 63
QY	3189	GTGCTGATCTGGGAAACCCCTGGCGGTACCCAACTTAATTCGCTTTGCAGCACATCCGCCCTT 3248
DB	64	GTGCTGATCTGGGAAACCCCTGGCGGTACCCCACTTAATTCGCTTTGCAGCACATCCGCCCTT 123
QY	3249	TGCGCAGCTGCGGTATAGAGAGAGAGCCCGCGACCGGATCGCCCTTCCCAACAGTTGCGCA 3308
DB	124	TGCGCAGCTGCGGTATAGAGAGAGAGCCCGCGACCGGATCGCCCTTCCCAACAGTTGCGCA 183
QY	3309	GCCTGAATGGCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGCTGTGGT 3368
DB	184	GCCTGAATGGCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGCTGTGGT 243
QY	3369	TACGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTTTTCGCTTTCTT 3428
DB	244	TACGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTTTTCGCTTTCTT 303
QY	3429	CCCTTCCTTTCTGCGCAGCTTGCAGCGCTTTCGCGCTTTCGCTTTCGCTTTCCTT 3488
DB	304	CCCTTCCTTTCTGCGCAGCTTGCAGCGCTTTCGCGCTTTCGCTTTCGCTTTCCTT 363
QY	3489	TTTAGGTTCCCGATTTAGAGCTTTAGGCACTTCAGGCACTTCGCGCAAAACTTGATTTGGGGA 3548
DB	364	TTTAGGTTCCCGATTTAGTGTCTTTAGCGCACTTCGCGCAAAACTTGATTTAGGGA 423
QY	3549	TGCTTTCAGCTAGTGGGCACTCGCCCTGATAGACGGTTTTTCGCGCTTTGCAGCTTGCAGTC 3608
DB	424	TGCTTTCAGCTAGTGGGCACTCGCCCTGATAGACGGTTTTTCGCGCTTTGCAGCTTGCAGTC 483
QY	3609	CAGCTTCTTTAATAGTGGACTCTGTTCGAACTGGAACAACTCAACCCCTATCTCGGT 3668
DB	484	CAGCTTCTTTAATAGTGGACTCTGTTCGAACTGGAACAACTCAACCCCTATCTCGGT 543
QY	3669	CTATTCCTTTGATTTATAGGGAATTTGCGGATTTTCGCGCTATTTGGTTAAATAATCAGCT 3728
DB	544	CTATTCCTTTGATTTATAGGGAATTTTCGCGATTTTCGCGCTATTTGGTTAAATAATCAGCT 603
QY	3729	GATTTAAACAAATTTAAACCGGAATTTAAACAAATTTAAACCGCTTTACAAATTTTCGCTGA 3788
DB	604	GATTTAAACAAATTTAAACCGGAATTTAAACAAATTTAAACCGCTTTACAAATTTTCGCTGA 661
QY	3789	TGCGGTATTTCTCTTACGATCTGTGCGGTATTTTCAACCGCATACAGTGGGCACTTT 3848
DB	662	TGCGGTATTTCTCTTACGATCTGTGCGGTATTTTCAACCGCATACAGTGGGCACTTT 720
QY	3849	TCGGGGAATTCGCGGGAACCCCTATTTGTTTATTTCTTAATACATTTCAAAATATGTA 3908
DB	721	TCGGGGAATTCGCGGGAACCCCTATTTGTTTATTTCTTAATACATTTCAAAATATGTA 780
QY	3909	TCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAGGAAGAGTAT 3968
DB	781	TCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAGGAAGAGTAT 840
QY	3969	GAGTATTCACATTTCCGTGTGCGCCCTATTTCCCTTTTTCGCGCATTTTTCGCTCTGT 4028
DB	841	GAGTATTCACATTTCCGTGTGCGCCCTATTTCCCTTTTTCGCGCATTTTTCGCTCTGT 900
QY	4029	TTTGTCTACCCAGAAACCGCTGGTGAAGTAAAGATGCTGAAGATCAGTGTGTCACG 4088
DB	901	TTTGTCTACCCAGAAACCGCTGGTGAAGTAAAGATGCTGAAGATCAGTGTGTCACG 960
QY	4089	AGTGGGTTACATCGAATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTTCGCCCCGA 4148
DB	961	AGTGGGTTACATCGAATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTTCGCCCCGA 1020

QY	4149	AGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCG 4208
DB	1021	AGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCG 1080
QY	4209	TATTGACGCGGCGCAAGAGCAACTCGTCCGCCCATACACTATTCTCAGAAATGACTTGGT 4268
DB	1081	TATTGACGCGGCGCAAGAGCAACTCGTCCGCCCATACACTATTCTCAGAAATGACTTGGT 1140
QY	4269	TGAGTACTCAACCACTGATCAAGAAAGCATCTTAOGATGGCATGACAGTAAGAGAAATATG 4328
DB	1141	TGAGTACTCAACCACTGATCAAGAAAGCATCTTAOGATGGCATGACAGTAAGAGAAATATG 1200
QY	4329	CAGTGTGCGCATTAACCATGATGATTAACACTTGGCGCCCACTTACTTCTGCAACAGATCGG 4388
DB	1201	CAGTGTGCGCATTAACCATGATGATTAACACTTGGCGCCCACTTACTTCTGCAACAGATCGG 1260
QY	4389	AGGACCGAAGGAGCTAAACCGCTTTTTCGCAACAACATGGGGGATCATGTAACTCGCCTTGA 4448
DB	1261	AGGACCGAAGGAGCTAAACCGCTTTTTCGCAACAACATGGGGGATCATGTAACTCGCCTTGA 1320
QY	4449	TCGTTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGAACACGATGCC 4508
DB	1321	TCGTTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGAACACGATGCC 1380
QY	4509	TGTAGCAATGGCAACAAACGTTGGCGGCAAACTATTAACTGGCGAACTACTTACTTAGCTTC 4568
DB	1381	TGTAGCAATGGCAACAAACGTTGGCGGCAAACTATTAACTGGCGAACTACTTACTTAGCTTC 1440
QY	4569	CGGCAACCAATTAATAGACTGGATGAGCGGATGAAGTTGACGAGGACCACTTCTGCGCTC 4628
DB	1441	CGGCAACCAATTAATAGACTGGATGAGCGGATGAAGTTGACGAGGACCACTTCTGCGCTC 1500
QY	4629	GGCCCTTCGCGCTGGCTGGTTTATTCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCG 4688
DB	1501	GGCCCTTCGCGCTGGCTGGTTTATTCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCG 1560
QY	4689	CGGTATCTGACGACCTGCGGCGCATGTTGTAAGCCCTCCCGTATCGTAGTTATCTACAC 4748
DB	1561	CGGTATCTGACGACCTGCGGCGCATGTTGTAAGCCCTCCCGTATCGTAGTTATCTACAC 1620
QY	4749	GACGGGAGTCAGGCAACTATGATGAAACGAATAGACAGATCGCTGAGATAGTGGCTC 4808
DB	1621	GACGGGAGTCAGGCAACTATGATGAAACGAATAGACAGATCGCTGAGATAGTGGCTC 1680
QY	4809	ACTGATTAAGCAATTTGTTAACTGTGACCAAGTTTACTCATATATACTTTTAGATGATTT 4868
DB	1681	ACTGATTAAGCAATTTGTTAACTGTGACCAAGTTTACTCATATATACTTTTAGATGATTT 1740
QY	4869	AAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGAC 4928
DB	1741	AAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATAATCTCATGAC 1800
QY	4929	CAAAATCCCTTAAACGTCAGTTTTCGTTCCACTGAGCGCTCAGACCCCGTAGAAAAGATCAA 4988
DB	1801	CAAAATCCCTTAAACGTCAGTTTTCGTTCCACTGAGCGCTCAGACCCCGTAGAAAAGATCAA 1860
QY	4989	AGGATCTTCTGAGATCTCTTTTTCGCGCGTAATCTGCTGCTGTGCAACAAACCAAAACC 5048
DB	1861	AGGATCTTCTGAGATCTCTTTTTCGCGCGTAATCTGCTGCTGTGCAACAAACCAAAACC 1920
QY	5049	ACGCTTACAGCGGTGTTTGTGTCGCGATCAAGAGCTTACCAACTCTTTTTCGAGGT 5108
DB	1921	ACGCTTACAGCGGTGTTTGTGTCGCGATCAAGAGCTTACCAACTCTTTTTCGAGGT 1980
QY	5109	AACTGGCTTCAGCAGAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCGGTAGTAGG 5168
DB	1981	AACTGGCTTCAGCAGAGCGCAGATACCAATACTGCTCTTCTAGTGTAGCGGTAGTAGG 2040
QY	5169	CCACCACTTCAAGAACTCTGTAGCAGCGCTTACATACCTGCTGCTCTCTCTCTCTCTCT 5228
DB	2041	CCACCACTTCAAGAACTCTGTAGCAGCGCTTACATACCTGCTGCTCTCTCTCTCTCTCT 2100

[illegible]

QY 5769 GCGCCCAATAGCAACCGCTCTCCCGCGCGTGGCGGATTCATTAATGCAG 5822
 DB 2641 GCGCCCAATAGCAACCGCTCTCCCGCGCGTGGCGGATTCATTAATGCAG 2694

RESULT 14
 ADA41728/c
 ID ADA41728 standard; DNA; 3404 BP.
 XX
 XX ADA41728;
 XX AC
 XX DT - 20-NOV-2003 (first entry)
 XX
 XX Plasmid pJO-20 DNA.
 DB
 XX RNA-dependent RNA polymerase; RdRP; plant virus; amplification system;
 KW ds; circular; cyclic.
 KW
 XX Synthetic.
 OS
 XX WO2003014366-A2.
 PN
 XX 20-FEB-2003.
 PD
 XX 29-JUL-2002; 2002WO-DE002863.
 PF
 XX 30-JUL-2001; 2001DE-01037444.
 PR
 XX (PROB-) PROBIOTEN AG.
 PA
 XX Sandig V, Jordan I;
 PI
 XX MPI; 2003-248302/24.
 DR
 XX
 XX Amplifying nucleic acid in animal cells, useful e.g. for gene therapy or
 PT vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus.
 PT
 XX
 PS Example 2; Page 37-38; 39pp; German.

This invention describes a novel method for amplifying nucleic acid in animal cells by introducing an RNA-dependent RNA polymerase (RdRP) and its associated promoters and cis-acting signals from a plant virus into the cells. RdRP is normally active in plant cells and the gene that encodes it can be recovered from such cells. Both the RdRP and the promoter are from plant viruses, particularly turnip crinkle virus and the amplified RNA is a modified satellite or genomic RNA of this virus. The method is particularly used for amplification of RNA (which may be mRNA for protein synthesis; an effector, e.g. antisense RNA or ribozyme, or genomic RNA) in animal cells, for (i) control of gene expression or (ii) for gene therapy or vaccination. When the system includes an inducible promoter, it permits strong and rapid expression of reporter genes in response to a test substance, especially where the promoter responds to the human immune deficiency virus or heavy metals, to produce a diagnostic system or biosensor, respectively. The method of the invention provides an inducible or constitutive, autonomous RNA-dependent RNA amplification system for animal cells that requires only one polymerase and does not use any viral structural genes or helper viruses. Amplification takes place in the cytoplasm without using any components potentially infectious for the host cells. Human 293 cells were transformed with (i) pJO-39, expressing a turnip crinkle virus 88 kD protein; (ii) pJO-60, expressed satellite RNA-C of the same virus in the sense orientation and a fusion of internal ribosome entry site and green fluorescent protein in the antisense orientation, and (iii) an expression vector for T7 RNA polymerase under control of the cytomegalovirus promoter. Expression of the reporter gene was detected by fluorescence microscopy. This sequence represents a fragment of plasmid, pJO-20 DNA used in the invention.

Sequence 3404 BP; 858 A; 853 C; 863 G; 830 T; 0 U; 0 Other;

Query Match 45.48; Score 2641.4; DB 8; Length 3404;
 Best Local Similarity 99.74; Pred. No. 0;

	Matches 2668;	Conservative	0;	Mismatches	6;	Indels	3;	Gaps	2;
QY	3146	TATAGTCAGTCGTATTACAAATTCCTGCGCGCTCGTTTACAAAGTCGTGAGCTGGGAAAC		3205					
DB	3404	TATAGTCAGTCGTATTACAAATTCCTGCGCGCTCGTTTACAAAGTCGTGAGCTGGGAAAC		3345					
QY	3206	CCTGGCGTTACCCCAACTTAATGCGCTTGCAGCAGCATCCCCCTTTCGCCAGCTGGCGTAAT		3265					
DB	3344	CCTGGCGTTACCCCAACTTAATGCGCTTGCAGCAGCATCCCCCTTTCGCCAGCTGGCGTAAT		3285					
QY	3266	AGCGAAGAGGCCCGCAGTCGCGCTTCCCAACAGTTTGGCGAGCTCTGAATGGCGAATGG		3325					
DB	3284	AGCGAAGAGGCCCGCAGTCGCGCTTCCCAACAGTTTGGCGAGCTCTGAATGGCGAATGG		3225					
QY	3326	ACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTTACGCGAGCGTGCAGCG		3385					
DB	3224	ACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTTACGCGAGCGTGCAGCG		3165					
QY	3386	CTACACTTGCAGCGCCCTAGCGCGCTCTTTCGGCTTCTCCCTTCTCTTCGCGCA		3445					
DB	3164	CTACACTTGCAGCGCCCTAGCGCGCTCTTTCGGCTTCTCTTCGCTTCTCTTCGCGCA		3105					
QY	3446	CGTTTCGCGCGCTTTCGCCCTTCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTA		3505					
DB	3104	CGTTTCGCGCGCTTTCGCCCTTCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTA		3045					
QY	3506	GAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTGGGTGATGGTTCAAGTGTGGC		3565					
DB	3044	GTGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTAGGGTGTGGTTCAAGTGTGGC		2985					
QY	3566	CATCGCCCTGATAGACGGTTTTCGCCCTTTCGCGCTTTCGAGCTTGGAGTCCAGCTTCTT		3625					
DB	2984	CATCGCCCTGATAGACGGTTTTCGCCCTTTCGAGCTTGGAGTCCAGCTTCTTAAATAGT		2925					
QY	3626	GACTCTTGTTCGCAACTGGAACACACTCAACCCCTATCTCGGTCTATCTTCTTTGATTTAT		3685					
DB	2924	GACTCTTGTTCGCAACTGGAACACACTCAACCCCTATCTCGGTCTATCTTCTTTGATTTAT		2865					
QY	3686	AAGGGATTTTCGCGATTTTCGCCCTTATTTGTTTAAATAAGTGTGATTTTAAATAATTTA		3745					
DB	2864	AAGGGATTTTCGCGATTTTCGCCCTTATTTGTTTAAATAAGTGTGATTTTAAATAATTTA		2805					
QY	3746	ACGCGAATTTTACAAATATTAAGTTTACAAATTTCCGCTGATGGCTATTTTCCTCTT		3805					
DB	2804	ACGCGAATTTTACAAATATTAAGTTTACAAATTTTCCTGATGGCTATTTTCCTCTT		2747					
QY	3806	ACGCACTCTGCGGTATTTTACACCGCATACAGGTGGCAGCTTTTCGGGGAATGTGCGCG		3865					
DB	2746	ACGCACTCTGCGGTATTTTACACCGCATACAGGTGGCAGCTTTTCGGGGAATGTGCGCG		2688					
QY	3866	GAACCCCTATTTGTTTATTTTCTAAATATCAATTCAAATATGATTCGCTCATGAGACAAAT		3925					
DB	2687	GAACCCCTATTTGTTTATTTTCTAAATATCAATTCAAATATGATTCGCTCATGAGACAAAT		2628					
QY	3926	AACCTGTATTAATGCTTCAATATATTTGAAAGGAGAGATGATGAGTATTCACATTTCC		3985					
DB	2627	AACCTGTATTAATGCTTCAATATATTTGAAAGGAGAGATGATGAGTATTCACATTTCC		2568					
QY	3986	GTGTCGCCCTTATTTTCCTTTTTCGCCCATTTTTCCTTCTCTGTTTTCCTCACCAGAAA		4045					
DB	2567	GTGTCGCCCTTATTTTCCTTTTTCGCCCATTTTTCCTTCTCTGTTTTCCTCACCAGAAA		2508					
QY	4046	CGCTGTGAAAGTAAAGATGCTGAAGATCAGTTTGGGTGACAGATGGGTACATCGAAC		4105					
DB	2507	CGCTGTGAAAGTAAAGATGCTGAAGATCAGTTTGGGTGACAGATGGGTACATCGAAC		2448					
QY	4106	TGATCTCAACAGCGGTAAAGATCTTTCGAGAGTTTTCGCCCGGAGAGAGCTTTTCCAAATGA		4165					
DB	2447	TGATCTCAACAGCGGTAAAGATCTTTCGAGAGTTTTCGCCCGGAGAGAGCTTTTCCAAATGA		2388					
QY	4166	TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATTTGACCGCGGCAAG		4225					
DB	2387	TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTATTTGACCGCGGCAAG		2328					

QY 4226 AGCAACTCGTCCGCGATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCAACGATCA 4285
DB 2327 AGCAACTCGTCCGCGCATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCAACGATCA 2268
QY 4286 CAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTTATCAGTGTGCCATACCA 4345
DB 2267 CAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTTATCAGTGTGCCATACCA 2208
QY 4346 TGAGTGATAACACTCGCGCCCAACTTTACTCTCGAACAGATCGGAGGACCGAAGGAGCTAA 4405
DB 2207 TGAGTGATAACACTCGCGCCCAACTTTACTCTCGAACAGATCGGAGGACCGAAGGAGCTAA 2148
QY 4406 CCGCTTTTTCACACATGCGGGGATCATGTAACTCGCTCTTGATCTGTTGGGAAACCGGAGC 4465
DB 2147 CCGCTTTTTCACACATGCGGGGATCATGTAACTCGCTCTTGATCTGTTGGGAAACCGGAGC 2088
QY 4466 TGAATGAAGCCATACCAAAACGACGAGGTGACACACGATGCTGTAGCAATGGCAACAA 4525
DB 2087 TGAATGAAGCCATACCAAAACGACGAGGTGACACACGATGCTGTAGCAATGGCAACAA 2028
QY 4526 CGTTGGCGAAACTATTAACATGCGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAG 4585
DB 2027 CGTTGGCGAAACTATTAACATGCGGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAG 1968
QY 4586 ACTGGATGAGGGCGGATTAAGTTGCGAGGACCACTTCTCGGCTCGGCCCTTCGCGCTGGCT 4645
DB 1967 ACTGGATGAGGGCGGATTAAGTTGCGAGGACCACTTCTCGGCTCGGCCCTTCGCGCTGGCT 1908
QY 4646 GGTTTATGCTGATAAATCTGAGGCGGTGAGGCTGGGTCTCGCGGTATCATTTGACGAC 4705
DB 1907 GGTTTATGCTGATAAATCTGAGGCGGTGAGGCTGGGTCTCGCGGTATCATTTGACGAC 1848
QY 4706 TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGAGGGGAGTCAGGCA 4765
DB 1847 TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGAGGGGAGTCAGGCA 1788
QY 4766 CTATGATGAACGAATAGACAGATCGTCGAGATAGTGCTCACTGATTAAGCATTTGCT 4825
DB 1787 CTATGATGAACGAATAGACAGATCGTCGAGATAGTGCTCACTGATTAAGCATTTGCT 1728
QY 4826 AACTGTCCAGACCAAGTTTACTCATATATCTTTAGATTGATTTAAACTTCATTTTAAAT 4885
DB 1727 AACTGTCCAGACCAAGTTTACTCATATATCTTTAGATTGATTTAAACTTCATTTTAAAT 1668
QY 4886 TTAAGAGGATCTAGGTGAAGATCCTTTTGTGATAATCTATGACCAAAATCCCTTAACGTG 4945
DB 1667 TTAAGAGGATCTAGGTGAAGATCCTTTTGTGATAATCTATGACCAAAATCCCTTAACGTG 1608
QY 4946 AGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAGAGATCAAGGATCTTCTTGAGTC 5005
DB 1607 AGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAGAGATCAAGGATCTTCTTGAGTC 1548
QY 5006 CTTTTTTTCTGCGGTAATCTGCTGTGTCGTAACAAACCAACCAACCAACCAACCAACCA 5065
DB 1547 CTTTTTTTCTGCGGTAATCTGCTGTGTCGTAACAAACCAACCAACCAACCAACCAACCA 1488
QY 5066 TTTGTTTTCGCGATCAAGAGTACCAACTCTTTTTCGAAAGGTAACCTGGCTTCAGCAGAG 5125
DB 1487 TTTGTTTTCGCGATCAAGAGTACCAACTCTTTTTCGAAAGGTAACCTGGCTTCAGCAGAG 1428
QY 5126 CCGAGATACCAATATCTGCTCTAGTGAGCGGTAGTGTAGGCCACCACTTCAAGACT 5185
DB 1427 CCGAGATACCAATATCTGCTCTAGTGAGCGGTAGTGTAGGCCACCACTTCAAGACT 1368
QY 5186 CTGTAGCACCGCTTACATACCTCGCTCTGCTATCTCTGTTACAGTGGCTGCTGCCAGTG 5245
DB 1367 CTGTAGCACCGCTTACATACCTCGCTCTGCTATCTCTGTTACAGTGGCTGCTGCCAGTG 1308
QY 5246 GCGATAGTGTCTTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGC 5305
DB 1307 GCGATAGTGTCTTTACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGC 1248

QY 5306 GGTCCGGCTGAACCGGGGTTCTGTGACACAGCCAGCTTGGAGCGAACGACCTACACCG 5365
DB 1247 GGTCCGGCTGAACCGGGGTTCTGTGACACAGCCAGCTTGGAGCGAACGACCTACACCG 1188
QY 5366 AACTGAGATACCTTACAGCGTGAGCTATGAGAAAGCGCACGCTTCCGAAAGGAGAAAGG 5425
DB 1187 AACTGAGATACCTTACAGCGTGAGCTATGAGAAAGCGCACGCTTCCGAAAGGAGAAAGG 1128
QY 5426 CCGACAGGTATCCGGTAAGCGGCGAGGTCGGAACAGAGAGCGCACGAGGAGCTTCCAG 5485
DB 1127 CCGACAGGTATCCGGTAAGCGGCGAGGTCGGAACAGAGAGCGCACGAGGAGCTTCCAG 1068
QY 5486 CCGGAAACCGCTGTATCTTATAGTCTGCTCGGGTTTCGACCTCTGACTTTGAGCGTC 5545
DB 1067 CCGGAAACCGCTGTATCTTATAGTCTGCTCGGGTTTCGACCTCTGACTTTGAGCGTC 1008
QY 5546 GATTTTGTGATGCTCGTCAAGGGGCGGAGCCCTATGGAAGAAACCGCAGCAACCGGCT 5605
DB 1007 GATTTTGTGATGCTCGTCAAGGGGCGGAGCCCTATGGAAGAAACCGCAGCAACCGGCT 948
QY 5606 TTTTACGGTTCTGGCTTTTGTCTGCGCTTTTGTCTCAGATTTCTTCTGCGTTATCCC 5665
DB 947 TTTTACGGTTCTGGCTTTTGTCTGCGCTTTTGTCTCAGATTTCTTCTGCGTTATCCC 888
QY 5666 CTGATTTCTGGATACCGTATTTACCGCTTTTGTGAGTGAGCTGATACCGCTCGCGCAGCC 5725
DB 887 CTGATTTCTGGATACCGTATTTACCGCTTTTGTGAGTGAGCTGATACCGCTCGCGCAGCC 828
QY 5726 GAACGACCGAGCGCAGCGAGTCACTGAGCGAGGAGCGAAGAGCGCCCAATACGCAAAC 5785
DB 827 GAACGACCGAGCGCAGCGAGTCACTGAGCGAGGAGCGAAGAGCGCCCAATACGCAAAC 768
QY 5786 CGCTCTCCCGCGCGTTGCGCGGATTCATTAATGCGAG 5822
DB 767 CGCTCTCCCGCGCGTTGCGCGGATTCATTAATGCGAG 731

RESULT 15
AAD09981/c
ID AAD09981 standard; DNA; 3968 BP.
XX
XX AAD09981;
AC
DT 12-SEP-2001 (first entry)
XX
DE pHP70-IMCS construct for transfection of pacific oysters.
XX
XX Fruitfly; fertility; reproduction; gametogenesis; microinjection; HSP;
KW infection; plasmid pHP70-IMCS; heat shock promoter; embryogenesis; da.
XX
OS Drosophila melanogaster.
OS Unidentified.
OS Chimeric.
XX
XX WO200148224-A1.
PN
PD 05-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-AU001596.
PF
XX
XX 24-DEC-1999; 99AU-00004884.
PR
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
PA
PI Threshner R, Hinds L, Hardy C, Whyard S, Vignarajan S, Grewe PM;
PI Patil J;
XX
XX WPI; 2001-425672/45.
DR
XX
PT Novel construct for preventing embryogenesis in animals comprises native
PT promoter, blocking DNA which abrogates function of crucial gene and
PT genetic switch to regulate expression/repression of blocker/gene
PT knockout.

XX	Example 9; Page 198-200; 241pp; English.	
PS	The invention relates to a construct which allows animals to be bred in	
XX	captivity but renders them infertile in the wild by allowing reversible	
CC	control over fertility and reproduction. The construct comprises a native	
CC	promoter, a blocking DNA sequence contoured for and designed to abrogate	
CC	a crucial gene's function or to cause its mis-expression, and a genetic	
CC	switch to regulate controlled expression/repression of the blocker/gene	
CC	knockout. The construct is useful for preventing embryogenesis or	
CC	gametogenesis in animals by stably transforming an animal cell with the	
CC	construct by microinjection, transfection or infection, where the	
CC	construct stably integrates into the genome by homologous recombination,	
CC	and implanting the cell into a host organism, where a whole animal	
CC	develops from the implanted cell. The present DNA sequence is plasmid	
CC	construct pHSF70-1MCS used for transfection of Pacific oysters. The	
CC	plasmid contains Drosophila heat shock promoter 70 (dHSP70) and its poly	
CC	adenylation signal	
XX	Sequence 3968 BP; 1075 A; 917 C; 943 G; 1033 T; 0 U; 0 Other;	
Query Match	45.2%; Score 2634.4; DB 4; Length 3968;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 2635; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
Qy	3187 ACCTGCTGACTGGGAAACCCCTGGCTTACCCAACTTAATCGCCTTGACGACATCCCCC	3246
Db		
Qy	3968 ACCTGCTGACTGGGAAACCCCTGGCTTACCCAACTTAATCGCCTTGACGACATCCCCC	3909
Db		
Qy	3247 TTTCCGACGCTGGGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCG	3306
Db		
Qy	3908 TTTCCGACGCTGGGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCG	3849
Db		
Qy	3307 CAGCCTCAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGGGGGGGTGTGGTG	3366
Db		
Qy	3848 CAGCCTCAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGGGGGGGTGTGGTG	3789
Db		
Qy	3367 GTTACGCGCAGCGTGAACGCTGACACTTGCAGCGCCCTAGCGCCGCTCTTTCGCTTTC	3426
Db		
Qy	3788 GTTACGCGCAGCGTGAACGCTGACACTTGCAGCGCCCTAGCGCCGCTCTTTCGCTTTC	3729
Db		
Qy	3427 TTTCCCTTCTTTCGCGCACGTTTCGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTC	3486
Db		
Qy	3728 TTTCCCTTCTTTCGCGCACGTTTCGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTC	3669
Db		
Qy	3487 CTTTATGGGTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGT	3546
Db		
Qy	3668 CTTTATGGGTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGT	3609
Db		
Qy	3547 GATGGTTTCACTAGTGGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTTGAAGTTGGAG	3606
Db		
Qy	3608 GATGGTTTCACTAGTGGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTTGAAGTTGGAG	3549
Db		
Qy	3607 TCCAGGTTCTTAATAGTGAAGCTTCTGTTCCAACTGGACCAACACTCAACCTTATCTCG	3666
Db		
Qy	3548 TCCAGGTTCTTAAATAGTGAAGCTTCTGTTCCAACTGGACCAACACTCAACCTTATCTCG	3489
Db		
Qy	3667 GTCTATTCTTTTCAATTAAGGATTTTTCGGGATTTTCGGGCTTATGGTTTAAAAAATGAG	3726
Db		
Qy	3488 GTCTATTCTTTTGAATTAAGGATTTTTCGGGATTTTCGGGCTTATGGTTTAAAAAATGAG	3429
Db		
Qy	3727 CTGATTTTAAACAAATATTAACGGCAATTTTAAACAAATATTAACGTTTACAAATTCGCCCT	3786
Db		
Qy	3428 CTGATTTTAAACAAATATTAACGGCAATTTTAAACAAATATTAACGTTTACAAATTCGCCCT	3369
Db		
Qy	3787 GATCGGATATTTCTTCAAGCATCTGTGGGATTTTCAACCGCATACAGGTGGCACT	3846
Db		
Qy	3368 GATCGGATATTTCTTCAAGCATCTGTGGGATTTTCAACCGCATACAGGTGGCACT	3309
Db		
Qy	3847 TTTTCGGGAAATGTCGGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATG	3906
Db		
Qy	3308 TTTTCGGGAAATGTCGGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAAAATATG	3249
Db		

Qy	3907 TATCGGCTCATGAGACATTAACCCCTGATAAANTGCTTCAATAATATTTGAAAAAGGAGACT	3966
Db		
Qy	3248 TATCGGCTCATGAGACATTAACCCCTGATAAANTGCTTCAATAATATTTGAAAAAGGAGACT	3189
Db		
Qy	3967 ATGAGTATTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGGGCAATTTTGCCTTCT	4026
Db		
Qy	3188 ATGAGTATTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGGGCAATTTTGCCTTCT	3129
Db		
Qy	4027 GTTTTTCCTCACCCAGAAACCTCGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCA	4086
Db		
Qy	3128 GTTTTTCCTCACCCAGAAACCTCGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCA	3069
Db		
Qy	4087 CGAGTGGTTTACATCGAATCTGATCTCAACAGCGTGAAGTCCCTTTGAGAGTTTTCGCCCC	4146
Db		
Qy	3068 CGAGTGGTTTACATCGAATCTGATCTCAACAGCGTGAAGTCCCTTTGAGAGTTTTCGCCCC	3009
Db		
Qy	4147 GAACAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTATATCC	4206
Db		
Qy	3008 GAACAACTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTATATCC	2949
Db		
Qy	4207 CGTATTGACGCGCGGCAAGACAACTCGGTCCGCGCATACACTATTTCTGAGAAATGACTTG	4266
Db		
Qy	2948 CGTATTGACGCGCGGCAAGACAACTCGGTCCGCGCATACACTATTTCTGAGAAATGACTTG	2889
Db		
Qy	4267 GTTTCAGTACTCACCAGTCAACAGAAAGCATCTTACGGATGCGATGACACAGTAAGAAATTA	4326
Db		
Qy	2888 GTTTCAGTACTCACCAGTCAACAGAAAGCATCTTACGGATGCGATGACACAGTAAGAAATTA	2829
Db		
Qy	4327 TGCAGTCTGTCATAAACCATGAGTGAATAACACTGCGGCCAACTTACTTCTGACAAACGATC	4386
Db		
Qy	2828 TGCAGTCTGTCATAAACCATGAGTGAATAACACTGCGGCCAACTTACTTCTGACAAACGATC	2769
Db		
Qy	4387 GGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAACATGCGGGGATCATGTAACTCGCCTT	4446
Db		
Qy	2768 GGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAACATGCGGGGATCATGTAACTCGCCTT	2709
Db		
Qy	4447 GATCGTTGGGAAACCGGAGCTGAATGAAGCCCATACCAACGACGAGCGTGACACCAAGATG	4506
Db		
Qy	2708 GATCGTTGGGAAACCGGAGCTGAATGAAGCCCATACCAACGACGAGCGTGACACCAAGATG	2649
Db		
Qy	4507 CCTGTAGCAATGGCAACAACTTTCGCGCAAACTTAACTGCGGCAACTTACTTACTTAGCT	4566
Db		
Qy	2648 CCTGTAGCAATGGCAACAACTTTCGCGCAAACTTAACTGCGGCAACTTACTTACTTAGCT	2589
Db		
Qy	4567 TCCCGGCAACAAATTAATAGACTGATGAGGCGGATTAAGTTTGACGAGCAACCTTCTGCGC	4626
Db		
Qy	2588 TCCCGGCAACAAATTAATAGACTGATGAGGCGGATTAAGTTTGACGAGCAACCTTCTGCGC	2529
Db		
Qy	4627 TCGGCCCTTCGGGCTGGCTGTTTATTCGATTAATCTGAGCGCGTGAGCGTGGGTCT	4686
Db		
Qy	2528 TCGGCCCTTCGGGCTGGCTGTTTATTCGATTAATCTGAGCGCGTGAGCGTGGGTCT	2469
Db		
Qy	4687 CGCGGTATCATTTGACGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTAC	4746
Db		
Qy	2468 CGCGGTATCATTTGACGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTAC	2409
Db		
Qy	4747 ACAGCGGGAGTCAAGCAACTATGATGAAACGAAATAGACAGATCGCTGAGATAGGTGCC	4806
Db		
Qy	2408 ACAGCGGGAGTCAAGCAACTATGATGAAACGAAATAGACAGATCGCTGAGATAGGTGCC	2349
Db		
Qy	4807 TCACGTGATTAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATCTTTAGATTGAT	4866
Db		
Qy	2348 TCACGTGATTAAGCATTTGGTAACTGTCAGACCAAGTTTACTCATATATATCTTTAGATTGAT	2289
Db		
Qy	4867 TTAACAACTTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCCTTTTGTAAATCTCATG	4926
Db		
Qy	2288 TTAACAACTTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCCTTTTGTAAATCTCATG	2229
Db		
Qy	4927 ACCAAATCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTGAAGATGATC	4986
Db		
Qy	2228 ACCAAATCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTGAAGATGATC	2169
Db		
Qy	4987 AAGGATCTCTTGAGATCTCTTTTCTGCGCGTAACTCTGCTGCTTCAACAAAAA	5046
Db		

Db	2168	AAAGGATCTTCTTGAGATCTTTTTTCTGCGGTAACTGCTGCTTGCAAAACAAAAA	2109
Qy	5047	CCACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTCCGAAG	5106
Db	2108	CCACCGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTCCGAAG	2049
Qy	5107	GTAACTGGCTTCAGCAGAGCGGAGATACCAAACTCTCTCTAGTGTAGCGGTAGTTA	5166
Db	2048	GTAACTGGCTTCAGCAGAGCGGAGATACCAAACTCTCTCTAGTGTAGCGGTAGTTA	1989
Qy	5167	GGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAACTCTGTTA	5226
Db	1988	GGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAACTCTGTTA	1929
Qy	5227	CCAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAG	5286
Db	1928	CCAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAG	1869
Qy	5287	TTACCGGATAAGCGCGAGCGGTGCGGCTGAAACGGGGGGTTCGTGCACACAGCCAGCTTG	5346
Db	1868	TTACCGGATAAGCGCGAGCGGTGCGGCTGAAACGGGGGGTTCGTGCACACAGCCAGCTTG	1809
Qy	5347	GAGCGACGACCTACACCGGACTGAGATACCTACAGCGTGGAGCTATCAGAAAGCGCCACG	5406
Db	1808	GAGCGACGACCTACACCGGACTGAGATACCTACAGCGTGGAGCTATCAGAAAGCGCCACG	1749
Qy	5407	CTTCCCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGACAGGGTCGGAAACAGGAGAG	5466
Db	1748	CTTCCCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGACAGGGTCGGAAACAGGAGAG	1689
Qy	5467	CGCACGAGGAGCTTCACGGGGGAAACGCGCTGGTATCTTTATAGTCTCTCGGGTTTCGC	5526
Db	1688	CGCACGAGGAGCTTCACGGGGGAAACGCGCTGGTATCTTTATAGTCTCTCGGGTTTCGC	1629
Qy	5527	CACCTCTGACTTGAGCGTTCGATTTTCTGTGATGCTCGTCAAGGGGCGGAGCCTATGAAA	5586
Db	1628	CACCTCTGACTTGAGCGTTCGATTTTCTGTGATGCTCGTCAAGGGGCGGAGCCTATGAAA	1569
Qy	5587	AACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGGCCCTTTTGTCTCACATG	5646
Db	1568	AACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCCTTTTGTGGCCCTTTTGTCTCACATG	1509
Qy	5647	TTCTTTCTCGGTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTTGAGTGAGCT	5706
Db	1508	TTCTTTCTCGGTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTTGAGTGAGCT	1449
Qy	5707	GATACCGCTCGCGCAGCGAAACGACGAGCGGAGTCAAGTACGAGGAGGAGCGGAA	5766
Db	1448	GATACCGCTCGCGCAGCGAAACGACGAGCGGAGTCAAGTACGAGGAGGAGCGGAA	1389
Qy	5767	GAGCGCCCAATACGCAACCGCTCTCCCGCGGTTGGCCGATTTCAATTAATGAG 5822	
Db	1388	GAGCGCCCAATACGCAACCGCTCTCCCGCGGTTGGCCGATTTCAATTAATGAG 1333	

Search completed: June 20, 2004, 10:58:48
Job time : 1995 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2004, 05:20:42 ; Search time 13309 Seconds
(without alignments)

13063.161 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagcagagtttccg.....tggcgcattcattaatgag 5822

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_eston.*
17: em_gss_hum.*
18: em_gss_in.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1055.8	18.1	1070	9	AJ281552 4AJA-P6F1
C 2	986.4	16.9	1013	12	BM438846 Iplvtr0015
C 3	924	15.9	1004	9	AJ281480 4AJA-P4G8
C 4	916.2	15.7	973	14	CD458281 Fg08_08h0

5	895.6	15.2	917	14	CD458286
6	873	15.0	935	12	BG838279
7	865.4	14.9	918	14	CD459092
8	841	14.4	841	9	AL042026
9	832.8	14.3	872	14	CD459085
10	825	14.2	1073	14	CF269652
11	824.6	14.2	854	12	BM438950
12	819.6	14.1	870	14	CD458333
13	815.6	14.0	1249	28	BZ572284
14	814.4	14.0	1126	28	BZ577702
15	808	13.9	819	14	CD649375
16	807.6	13.9	966	28	BZ570738
17	801.6	13.8	1483	28	BZ575896
18	797.6	13.7	1011	28	BZ576726
19	785.4	13.5	1574	28	BZ572566
20	777.8	13.4	800	9	AJ281449
21	777.6	13.4	910	14	CD649387
22	774.8	13.3	1336	28	BZ575810
23	774.4	13.3	789	14	CD280920
24	772.4	13.3	954	9	AL044364
25	771.8	13.3	1067	9	AU081137
26	770.4	13.2	1370	28	BZ571721
27	763.2	13.1	780	13	BQ825693
28	757	13.0	759	14	CD279661
29	755.4	13.0	1463	28	BZ571475
30	753.6	12.9	797	12	BM410796
31	745.4	12.8	786	14	CD458721
32	745.4	12.8	844	28	BZ574513
33	743.6	12.8	832	12	BG923768
34	741	12.7	741	14	CD279174
35	741	12.7	966	28	BZ575002
36	740.4	12.7	1089	9	AU081124
37	739.8	12.7	1003	28	BZ576686
38	739.8	12.7	1112	28	BZ577534
39	739.2	12.7	914	28	BZ569398
40	738.6	12.7	863	14	CF752100
41	733.8	12.6	950	28	BZ571129
42	733.2	12.6	811	29	ATH517156
43	732.4	12.6	998	28	BZ576702
44	732.4	12.6	1376	28	BZ571741
45	730	12.5	730	14	CD281097

ALIGNMENTS

RESULT 1	AJ281552	1070 bp	mRNA	linear	EST 30-JUN-2000
LOCUS	4AJA-P6F11-P	Anopheles gambiae	immune competent	4AJA	Anopheles
DEFINITION	gambiae cDNA clone 4AJA-P6F11, mRNA sequence.				
ACCESSION	AJ281552				
VERSION	AJ281552.1	GI:6929432			
KEYWORDS	EST.				
SOURCE	Anopheles gambiae	(African malaria mosquito)			
ORGANISM	Anopheles gambiae				
REFERENCE	1 (bases 1 to 1070)				
AUTHORS	Dinopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C., Donohue,M., Schultz,J., Benes,V., Bork,P., Ansoorge,W., Soares,M.B. and Kafatos,F.C.				
TITLE	Anopheles gambiae pilot gene discovery project: Identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (12),	6619-6624	(2000)	
MEDLINE	20300950				
PUBMED	10841561				
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany.				

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  source      Location/Qualifiers
1..1070      /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4A r/z"
/db_xref="taxon:7165"
/clone="4A3A-P6P11"
/cell_lines="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."
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ORIGIN

Query Match 18.1%; Score 1055.8; DB 9; Length 1070;
Best Local Similarity 99.7%; Pred. No. 2.1e-256;
Matches 1068; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

4527 GTTGGCGCAAACTATTACTGCGGAACCTACTTACTCTAGCTTCCCGGCAACAATTAAAGA 4586
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1070 GTTGGCGCAAACTATTAACTGCGGAACCTACTTACTCTAGCTTCCCGGCAACAATTAAAGA 1011
Qy |||||||
4587 CTGATGAGCGCGATAAAGTTGACGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTG 4646
Db |||||||
1010 CTGATGAGCGCGATAAAGTTGACGACCACTTCTGCGCTCGG-CTTCCGGCTGGCTG 952
Qy |||||||
4647 GTTTATTGCTGATAAATCTTGAGCGCGGTGAGCGGTGCTCGCGTATCATTTGAGCACT 4706
Db |||||||
951 GTTTATTGCTGATAAATCTTGAGCGCGGTGAGCGGTGCTCGCGTATCATTTGAGCACT 892
Qy |||||||
4707 GGGCCAGATGTTAAGCCCTCCGATGCTAGTTATCTACGACGCGGGAGTCAGGCAAC 4766
Db |||||||
891 GGGCCAGATGTTAAGCCCTCCGATGCTAGTTATCTACGACGCGGGAGTCAGGCAAC 832
Qy |||||||
4767 TATGATGAACCAATATAGACAGATCGCTGAGATAGGTGCGCTCACTGATTAAGCATTTGTA 4826
Db |||||||
831 TATGATGAACCAATATAGACAGATCGCTGAGATAGGTGCGCTCACTGATTAAGCATTTGTA 772
Qy |||||||
4827 ACTGTCAGACCAAGTTTACTCATATATCTTATAGATTTAAATTTAAATTTAAATTTAAAT 4886
Db |||||||
771 ACTGTCAGACCAAGTTTACTCATATATCTTATAGATTTAAATTTAAATTTAAATTTAAAT 712
Qy |||||||
4887 TAAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACGTGA 4946
Db |||||||
711 TAAAGGATCTAGTGAAGATCTTTTGTATATCTCATGACCAAAATCCCTTAACGTGA 652
Qy |||||||
4947 GTTTTCCTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCC 5006
Db |||||||
651 GTTTTCCTTCACCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCC 592
Qy |||||||
5007 TTTTTCCTTCAGCGTAACTGCTGCTGTCGAAACCAAAACCAACCGCTACAGCGGTGGT 5066
Db |||||||
591 TTTTTCCTTCAGCGTAACTGCTGCTGTCGAAACCAAAACCAACCGCTACAGCGGTGGT 532
Qy |||||||
5067 TTGTTTCGCGATCAAGAGCTACCAACTTTTTCGAGGATGATCTTCTGAGGATCTTCTGAGCAGC 5126
Db |||||||
531 TTGTTTCGCGATCAAGAGCTACCAACTTTTTCGAGGATGATCTTCTGAGGATCTTCTGAGCAGC 472
Qy |||||||
5127 GCAGATACCAAACTCTCTCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACTC 5186
Db |||||||
471 GCAGATACCAAACTCTCTCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAGAACTC 412
Qy |||||||
5187 TGTAGCACCGCTTACATACCTGCTCTGCTTAATCTGTTTACAGTGTGCTGCGCATGG 5246
Db |||||||
411 TGTAGCACCGCTTACATACCTGCTCTGCTTAATCTGTTTACAGTGTGCTGCGCATGG 352
Qy |||||||
5247 CGATAAGTCGTGCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAGGCGCAGCG 5306

351 CGATAAGTCGTGCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAGGCGCAGCG 292
Qy |||||||
5307 GTGCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGAGCGAAAGACCTACACCGA 5366
Db |||||||
291 GTGCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGAGCGAAAGACCTACACCGA 232
Qy |||||||
5367 ACTGATATACCTACAGCTGAGCTATGAGAAAGCGCCACCGTTCGGAAGGAGAAAGGC 5426
Db |||||||
231 ACTGATATACCTACAGCTGAGCTATGAGAAAGCGCCACCGTTCGGAAGGAGAAAGGC 172
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5427 GGACAGGTATCCGTTAGCGCGCAGGTCGGAACAGGAGCGACAGAGGAGCTTCCAGG 5486
Db |||||||
171 GGACAGGTATCCGTTAGCGCGCAGGTCGGAACAGGAGCGACAGAGGAGCTTCCAGG 112
Qy |||||||
5487 GGGAAACCGCTGCTATCTTTATAGTCTCTGCGGGTTCCGCCACCTCTGACTTGGAGCTG 5546
Db |||||||
111 GGGAAACCGCTGCTATCTTTATAGTCTCTGCGGGTTCCGCCACCTCTGACTTGGAGCTG 52
Qy |||||||
5547 ATTTTGTGATGCTCTGTCAGCGGGCGGAGCTATGGAAGAAACGCCAGCAA 5597
Db |||||||
51 ATTTTGTGATGCTCTGTCAGCGGGCGGAGCTATGGAAGAAACGCCAGCAA 1

RESULT 2
BM438846
LOCUS
DEFINITION Iplvr00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
1013 bp linear EST 31-JAN-2002
sequence.
BM438846
VERSION
BM438846.1 GI:18460568
KEYWORDS
EST.
SOURCE
Ictalurus punctatus (channel catfish)
ORGANISM
Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
REFERENCE
1 (bases 1 to 1013)
Pang, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.
Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@aesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
1..1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cDNA library"
/notes="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

FEATURES
source
1..1013
/organism="Ictalurus punctatus"
/mol_type="mRNA"
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/notes="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

ORIGIN
Query Match 16.9%; Score 986.4; DB 12; Length 1013;
Best Local Similarity 99.5%; Pred. No. 8.6e-239;
Matches 1009; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

4012 GCATTTTGGCTCTCTGTTTGTCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAA 4071
Db |||||||
1 GCATTTTGGCTCTCTGTTTGTCTCACCAGAGAGCGTGGTGAAGTAAAGATGCTGAA 60
Qy |||||||
4072 GATCAGTTGGGTGACGAGTGGGTATCATCTGAACTCTCAACAGCGGTAAGATCCTT 4131
Db |||||||
61 GATCAGTTGGGTGACGAGTGGGTATCATCTGAACTCTCAACAGCGGTAAGATCCTT 120


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Db 531 TTTTTCGAGAGTAATCGGCTTCAGCAGAGCGGAGATACCAATACTGTTCTTCTAGTGT 472
Qy 5156 AGCGGTAGTATAGGACACACCTTCAAGAACTCTGTAGACACCGCTACATACCTCGTCTGCG 5215
Db 471 AGCGGTAGTATAGGACACACCTTCAAGAACTCTGTAGACACCGCTACATACCTCGTCTGCG 412
Qy 5216 TAATCCTGTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTGTCTTTACCGGGTTGGACT 5275
Db 411 TAATCCTGTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTGTCTTTACCGGGTTGGACT 352
Qy 5276 CAAGCAGATAGTACCGGATAAGCGGACGCGTGGCGTGAACGGGGGTTGCTGCGACAC 5335
Db 351 CAAGCAGATAGTACCGGATAAGCGGACGCGTGGCGTGAACGGGGGTTGCTGCGACAC 292
Qy 5336 AGCCGAGCTTCGAGGACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAG 5395
Db 291 AGCCGAGCTTCGAGGACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAG 232
Qy 5396 AAAGCGCACCGCTTCCCGAAGGAGAGAGCGGACGAGTATCCGGTAAGCGGCGAGTGG 5455
Db 231 AAAGCGCACCGCTTCCCGAAGGAGAGAGCGGACGAGTATCCGGTAAGCGGCGAGTGG 172
Qy 5456 GAACGAGAGCGGACGAGGAGCTTCCAGGCGGAGAAACCGCTGATCTTTATAGTCCGTG 5515
Db 171 GAACGAGAGCGGACGAGGAGCTTCCAGGCGGAGAAACCGCTGATCTTTATAGTCCGTG 112
Qy 5516 TCGGCTTTCGCCACTCTGACTGAGCGTCCGATTTTGTGATGCTCGTCAGCGGGCGGA 5575
Db 111 TCGGCTTTCGCCACTCTGACTGAGCGTCCGATTTTGTGATGCTCGTCAGCGGGCGGA 52
Qy 5576 GCCTATGAGAAACGCCAGCAACCGCGGCTTTTACGGTTCTCGGCTTTT 5626
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RESULT 4

CD458281
LOCUS
DEFINITION
Fg08_08h09 R Fg08 AAFPC ECORC Fusarium graminearum complex substrate
Gibberella zeae cDNA clone Fg08_08h09, mRNA sequence.

CD458281
VERSION
KEYWORDS
SOURCE
ORGANISM
Gibberella zeae
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE
AUTHORS
1 (bases 1 to 973)
Watson, R.J., Heys, R., Chapados, J., Couroux, P., Harris, L.J.,
Hattori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A.,
Sprott, D. and Tinker, N.A.

TITLE
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate

JOURNAL
COMMENT
Unpublished (2003)
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA

Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES
source

1. 973
Location/Qualifiers
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/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_08h09"
/tissue type="Mycelium"
/dev stage="Asexual"
/lab_host="E. coli DH10B"

/clone_lib="Fg08_AAFPC_ECORC_Fusarium_graminearum_complex_s
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/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."

ORIGIN

	Query Match	15.7%	Score 916.2;	DB 14;	Length 973;
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Qy	3893	TACATTCAATATGTATCCGCTCATGAGCAATAACCCCTGATAAATGCTTCAATAATAT	3952		
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Db	144	GAATAAGGAAAGATATGAGTATTCACATTTTCGGTGTCCGCTTATTCCTTTTTCGGG	203		
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Db	204	CATTTCGCTTCTCTGTTTTCGCTCACCCAGAAACGCTGGTGAAGTAAAGTCTGAG	263		
Qy	4073	ATCAGTTGGGTGACAGGTTGATCTCAATCGAATCTCAACAGCGGTAGAGTCTTTG	4132		
Db	264	ATCAGTTGGGTGACAGGTTGATCTCAATCGAATCTCAACAGCGGTAGAGTCTTTG	323		
Qy	4133	AGAGTTTTCGCCCCGAGAAACGTTTTCATATGATGAGCACTTTTAAAGTTCTGCTATGTG	4192		
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Qy	4193	CGCGGCTATATCCGCTATTCAGCGCGGGAAGAGCAACTCGTCCGCGCATACACTATT	4252		
Db	384	CGCGGCTATATTCGCTATTCAGCGCGGGAAGAGCAACTCGTCCGCGCATACACTATT	443		
Qy	4253	CTCAGATGACTCTGCTTGGTGTACTCACCAGTCAACAGAAAGCATCTTACGGATGCGATGA	4312		
Db	444	CTCAGATGACTCTGCTTGGTGTACTCACCAGTCAACAGAAAGCATCTTACGGATGCGATGA	503		
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Db	504	CAGTAAGAGAAATATGCAAGTCTGCCATAACCATGAGTGATTAACACTCGGCGCAACTTAC	563		
Qy	4373	TTCTGACACAGTTCGGAGGACCGAAGGAGCTTAAACCGCTTTTTCGACACATGCGGGATC	4432		
Db	564	TTCTGACACAGTTCGGAGGACCGAAGGAGCTTAAACCGCTTTTTCGACACATGCGGGATC	623		
Qy	4433	ATGTAACTCGCCTTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGC	4492		
Db	624	ATGTAACTCGCCTTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGC	683		
Qy	4493	GTGACACACAGTTCGCTGATGCAATATGCGCAACAAAGTTCGCGCAAACTATTACTGCGGAC	4552		
Db	684	GTGACACACAGTTCGCTGATGCAATATGCGCAACAAAGTTCGCGCAAACTATTACTGCGGAC	743		
Qy	4553	TACTTACTCTAGCTTCCGCGCAACAAATTAATAGACTGGATGAGCGGATTAAGTTGAG	4612		
Db	744	TACTTACTCTAGCTTCCGCGCAACAAATTAATAGACTGGATGAGCGGATTAAGTTGAG	803		
Qy	4613	GACCACCTTCGCGCTCGGCCCTTCGCGCTGCTGCTTTTATTTGCTGATAAATCTGGAGCG	4672		
Db	804	GACCACCTTCGCGCTCGGCCCTTCGCGCTGCTGCTTTTATTTGCTGATAAATCTGGAGCG	863		
Qy	4673	GTGAGCTTGGGTCTCGCGGTATTCATTTGAGCACTTGGGGCGAGATGATGAGCTTCCCGTA	4732		
Db	864	GTGAGCTTGGGTCTCGCGGTATTCATTTGAGCACTTGGGGCGAGATGATGAGCTTCCCGTA	922		
Qy	4733	TCGTAGTTTATCTACACGACGGGGAGTCAGGCAACTATGATGAACGAATA	4783		

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923 TCGTAGTATACACGAGGGGAGTCAGGCAACTATGATGACGAATAGA 973

RESULT 5
CD458286                                917 bp    mRNA    linear    EST 03-JUN-2003
LOCUS                                     917 bp    mRNA    linear    EST 03-JUN-2003
DEFINITION Fg08_09a03_R Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate
Gibberella zeae cDNA clone Fg08_09a03, mRNA sequence.
ACCESSION CD458286
VERSION
KEYWORDS CD458286.1 GI:31373026
SOURCE
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 917)
AUTHORS Watson,R.J., Heya,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
TITLE A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
JOURNAL Unpublished (2003)
COMMENT Contact: Watson, Robert J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES
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XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."

ORIGIN
Query Match 15.2%; Score 885.6; DB 14; Length 917;
Best Local Similarity 99.6%; Pred. No. 3.2e-213;
Matches 886; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3833 ATACAGGTGGACATTTTCGGGGAATGTGGCGGAACCCCTATTGTTGTTTCTTCTAAA 3892
DB 26 ATTTAGTGGGACATTTTCGGGGAATGTGGCGGAACCCCTATTGTTGTTTCTTCTAAA 85
QY 3893 TACATTCAAATATGATCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATT 3952
DB 86 TACATTCAAATATGATCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATT 145
QY 3953 GAAAAAGAGAGATGATGATTCACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGG 4012
DB 146 GAAAAAGAGAGATGATGATTCACATTTCCGTGTGCGCCCTATTCCCTTTTTCGGG 205
QY 4013 CATTTTCCTTCCTGTTTTCCTCACCAGAAAGCTGGTGAAGATGAAGATCTGAAG 4072
DB 206 CATTTTCCTTCCTGTTTTCCTCACCAGAAAGCTGGTGAAGATGAAGATCTGAAG 265
QY 4073 ATCAGTTGGGTGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTGAAGATCCTTG 4132
DB 266 ATCAGTTGGGTGACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGGTGAAGATCCTTG 325

4133 AGAGTTTTCGCGCCGGAAGACGTTTTCGAATGATGAGCACCTTTTAAAGTTCTGCTATGTG 4192
DB 326 AGAGTTTTCGCGCCGGAAGACGTTTTCGAATGATGAGCACCTTTTAAAGTTCTGCTATGTG 385
QY 4193 GCGCGGTATTATCCGTTATTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATT 4252
DB 386 GCGCGGTATTATCCGTTATTGACGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATT 445
QY 4253 CTCAGAATGACTTGGTTGAGTACTCACAGTACACAGAAAAGCATCTTACGAGATGGATCA 4312
DB 446 CTCAGAATGACTTGGTTGAGTACTCACAGTACACAGAAAAGCATCTTACGAGATGGATCA 505
QY 4313 CAGTAAGAGANTATTGCAAGTCTGCCATAACCATGAGTGAATAACACTGGGCGCAACTTAC 4372
DB 506 CAGTAAGAGANTATTGCAAGTCTGCCATAACCATGAGTGAATAACACTGGGCGCAACTTAC 565
QY 4373 TTCTGACAAACGATCGGAGGACCGAAGAGACTAAACCGCTTTTTCGCAACACTGGGGGATC 4432
DB 566 TTCTGACAAACGATCGGAGGACCGAAGAGACTAAACCGCTTTTTCGCAACACTGGGGGATC 625
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DB 626 ATGTAACCTGCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGAGGAC 685
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DB 686 GTGACACCAAGATCGCTGTAGCAATGCAACAAAGTTCGCGCAAACTATTAACTGGCGAC 745
QY 4553 TACTTACTCTAGCTTTCGCGCAACAAATTAATAGACTGATGAGCGGAGTAAAGTTGCAG 4612
DB 746 TACTTACTCTAGCTTTCGCGCAACAAATTAATAGACTGATGAGCGGAGTAAAGTTGCAG 805
QY 4613 GACCATTCTGCGCTCGCGCCCTTCGCGCTGCGTGTGTTTATTCGTGATAAATCTGAGCGG 4672
DB 806 GACCATTCTGCGCTCGCGCCCTTCGCGCTGCGTGTGTTTATTCGTGATAAATCTGAGCGG 865
QY 4673 GTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGCGCAGATGGTAAGCC 4724
DB 866 GTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGCGCAGATGGTAAGCC 917

RESULT 6
BG838279                                935 bp    mRNA    linear    EST 25-MAY-2001
LOCUS                                     935 bp    mRNA    linear    EST 25-MAY-2001
DEFINITION Gc01_10e07_R Gc01_AAPC_ECORC_cold stressed Glycine clandestina
Glycine clandestina cDNA clone Gc01_10e07, mRNA sequence.
ACCESSION BG838279
VERSION
KEYWORDS BG838279.1 GI:14204601
SOURCE
ORGANISM Glycine clandestina
Glycine clandestina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 935)
AUTHORS Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
Tinker,N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Glycine clandestina
Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
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Site 2: XhoI; Plants incubated at 2 degrees under 12 hours
of light/day. Harvested after only 2-3 days of cold
treatment. cDNA was prepared with the Uni-Zap cDNA kit
from Stratagene. Eco RI adapters were linked followed by
digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN
Query Match 15.0%; Score 873; DB 12; Length 935;
Best Local Similarity 97.9%; Pred. No. 5.1e-210;
Matches 878; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

QY 3833 ATACAGTGGCCTTTTCGGGGAATGTGCGGGAACCCCTATTTCTTTTCTTAA 3892
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32 ATTTAGTGGCCTTTTCGGGGAATGTGCGGGAACCCCTATTTCTTTTCTTAA 91
QY 3893 TACATTCAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATT 3952
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
92 TACATTCAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATT 151
QY 3953 GAAAAAGGAGATGATGAGTATTCAACATTTCCGTGCGCCCTTATTCCTTTTGGCG 4012
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
152 GAAAAAGGAGATGATGAGTATTCAACATTTCCGTGCGCCCTTATTCCTTTTGGCG 211
QY 4013 CATTTTGCCTTCTGTTTTTGTCTACCCGAGAACCGCTGGTGAAGTAAAGATGCTGAAG 4072
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
212 CATTTTGCCTTCTGTTTTTGTCTACCCGAGAACCGCTGGTGAAGTAAAGATGCTGAAG 271
QY 4073 ATCAGTTGGGTGACAGAGTGGTTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTG 4132
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
272 ATCAGTTGGGTGACAGAGTGGTTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTG 331
QY 4133 AGAGTTTTCGCCCCGGAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTTGTCTATGTG 4192
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
332 AGAGTTTTCGCCCCGGAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTTGTCTATGTG 391
QY 4193 GCGCGTATATCCGCTATTTAGCGCGGCAAGAGCAATCGTGTCCGCCATACATATT 4252
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392 GCGCGTATATCCGCTATTTAGCGCGGCAAGAGCAATCGTGTCCGCCATACATATT 451
QY 4253 CTCAGAAATGACTTGGTTGAGTACTCTACCAAGTACAGAAAAGCAATCTTACGGATGCGCATGA 4312
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
452 CTCAGAAATGACTTGGTTGAGTACTCTACCAAGTACAGAAAAGCAATCTTACGGATGCGCATGA 511
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512 CAGTAAGAGAAATPATCAGTGTGCTCCATTAACCATGATGATACATCTGCGGCGCCAACTTA 571
QY 4372 CTTCTGACAAAGATCGAGGACCGAAGAGCTAACCGCTTTTTCGACAAACATGGGGAT 4431
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
572 CTTCTGACAAAGATCGAGGACCGAAGAGCTAACCGCTTTTTCGACAAACATGGGGAT 631
QY 4432 CATGTAATCGCTTGTATCGTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 4491
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692 CGTGACACCAAGATGCTGTAGCAATGGCAACAAACGTTGCGCAAACTTAACTTGGCGAA 751
QY 4552 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGATCTGATGAGGCGGATTAAGTTGCA 4611
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752 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGATCTGATGAGGCGGATTAAGTTGCA 811
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Site 2: XhoI; Plants incubated at 2 degrees under 12 hours
of light/day. Harvested after only 2-3 days of cold
treatment. cDNA was prepared with the Uni-Zap cDNA kit
from Stratagene. Eco RI adapters were linked followed by
digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN
Query Match 15.0%; Score 873; DB 12; Length 935;
Best Local Similarity 97.9%; Pred. No. 5.1e-210;
Matches 878; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

QY 3833 ATACAGTGGCCTTTTCGGGGAATGTGCGGGAACCCCTATTTCTTTTCTTAA 3892
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 ATTTAGTGGCCTTTTCGGGGAATGTGCGGGAACCCCTATTTCTTTTCTTAA 91
QY 3893 TACATTCAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATT 3952
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
92 TACATTCAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATATATT 151
QY 3953 GAAAAAGGAGATGATGAGTATTCAACATTTCCGTGCGCCCTTATTCCTTTTGGCG 4012
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
152 GAAAAAGGAGATGATGAGTATTCAACATTTCCGTGCGCCCTTATTCCTTTTGGCG 211
QY 4013 CATTTTGCCTTCTGTTTTTGTCTACCCGAGAACCGCTGGTGAAGTAAAGATGCTGAAG 4072
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
212 CATTTTGCCTTCTGTTTTTGTCTACCCGAGAACCGCTGGTGAAGTAAAGATGCTGAAG 271
QY 4073 ATCAGTTGGGTGACAGAGTGGTTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTG 4132
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272 ATCAGTTGGGTGACAGAGTGGTTTACATCGAATCGATCTCAACAGCGTGAAGATCCTTG 331
QY 4133 AGAGTTTTCGCCCCGGAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTTGTCTATGTG 4192
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332 AGAGTTTTCGCCCCGGAAGACGTTTTTCCAATGATGAGCACTTTTAAAGTTTGTCTATGTG 391
QY 4193 GCGCGTATATCCGCTATTTAGCGCGGCAAGAGCAATCGTGTCCGCCATACATATT 4252
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392 GCGCGTATATCCGCTATTTAGCGCGGCAAGAGCAATCGTGTCCGCCATACATATT 451
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DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
452 CTCAGAAATGACTTGGTTGAGTACTCTACCAAGTACAGAAAAGCAATCTTACGGATGCGCATGA 511
QY 4313 CAGTAAGAGAAATPATCAGTGTGCTCCATTAACCATGATGATACATCTGCGG-CCAACTTA 4371
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512 CAGTAAGAGAAATPATCAGTGTGCTCCATTAACCATGATGATACATCTGCGGCGCCAACTTA 571
QY 4372 CTTCTGACAAAGATCGAGGACCGAAGAGCTAACCGCTTTTTCGACAAACATGGGGAT 4431
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 4432 CATGTAATCGCTTGTATCGTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 4491
DB |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
632 CATGTAATCGCTTGTATCGTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 691
QY 4492 CGTGACACCAAGATGCTGTAGCAATGGCAACAAACGTTGCGCAAACTTAACTTGGCGAA 4551
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692 CGTGACACCAAGATGCTGTAGCAATGGCAACAAACGTTGCGCAAACTTAACTTGGCGAA 751
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752 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGATCTGATGAGGCGGATTAAGTTGCA 811
QY 4612 GGACCACTTCTGCGCTCGGCCCTTCGCGCTGGCTGTTTATTGCTGATAAATCTGAGGCG 4671
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Db 324 AGAGTTTTCGCCCGGAGAAAGTTCCTCAATGATGAGCAGCTTTTAAAGTTCCTGATGTG 383
Qy 4193 GCGCGGTATTATCCCGTATTGACCGCGGGGCAAGAGCACTCGGTGCGGCGATACACTATT 4252
Db 384 GCGCGGTATTATCCCGTATTGACCGCGGGGCAAGAGCACTCGGTGCGGCGATACACTATT 443
Qy 4253 CTCAGAATGACTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 4312
Db 444 CTCAGAATGACTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 503
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Qy 4492 CGTGACACACGATGCTGTAGCAATGGCAACCAACGTTGGCGAACTATTAACTGGCGAA 4551
Db 684 CGTGACACACGATGCTGTAGCAATGGCAACCAACGTTGGCGAACTATTAACTGGCGAA 743
Qy 4552 CTACTTACTTACTGCTTCCGCGCAACCAATTAATAGACTGGAGGCGGATTAAGTTGCA 4611
Db 744 CTACTTACTTACTGCTTCCGCGCAACCAATTAATAGACTGGAGGCGGATTAAGTTGCA 803
Qy 4612 GGACCACTTCTGCGCTCGGCGCTTCCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 4671
Db 804 GGACCACTTCTGCGCTCGGCGCTTCCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 863
Qy 4672 GGTGAGCGTGGGTCTCGCGGT-ATCATTGACGACACTGGGCGAGATGGTAAGGCC 4725
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RESULT 8
AL042026
LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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DKFZp434E111-5', mRNA sequence.
AL042026
AL042026.1 GI:5421372
EST.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
Poustka,A., Klein,M., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Poustka, et al.)
Unpublished (1999)
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZp434E111) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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ORIGIN
Query Match 14.4%; Score 841; DB 9; Length 841;
Best Local Similarity 100.0%; Pred. No. 6.7e-202;
Matches 841; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3873 TATTGTTTATTTTCTTAATACATTCAAATATGATGATCGGCTCATGAGACAATAACCTGT 3932
Db 1 TATTGTTTATTTTCTTAATACATTCAAATATGATGATCGGCTCATGAGACAATAACCTGT 60
Qy 3933 ATAAATGCTTCAATATATTTGAAAAGGAGAGATATGAGTATTCACATTTTCGGTGTGCG 3992
Db 61 ATAAATGCTTCAATATATTTGAAAAGGAGAGATATGAGTATTCACATTTTCGGTGTGCG 120
Qy 3993 CTTTATTTCCCTTTTTCGGGCAATTTTGGCTTCTCTGTTTTCCTCACCAGAAACGCTGT 4052
Db 121 CTTTATTTCCCTTTTTCGGGCAATTTTGGCTTCTCTGTTTTCCTCACCAGAAACGCTGT 180
Qy 4053 GAAAGTAAAGATGCTCAAGATCAGTTGGGTGACAGAGTGGTTTACATCGAACTGATCT 4112
Db 181 GAAAGTAAAGATGCTCAAGATCAGTTGGGTGACAGAGTGGTTTACATCGAACTGATCT 240
Qy 4113 CAACAGCGGTAAAGATCTTCAGAGTGTTCGCCCGGAGAAAGCGTTTTCCAATGATGAGCAC 4172
Db 241 CAACAGCGGTAAAGATCTTCAGAGTGTTCGCCCGGAGAAAGCGTTTTCCAATGATGAGCAC 300
Qy 4173 TTTTAAAGTTCTGCTATGTCGCGGTATTATTCGGTATTGACCGCGGGGCAAGCAACT 4232
Db 301 TTTTAAAGTTCTGCTATGTCGCGGTATTATTCGGTATTGACCGCGGGGCAAGCAACT 360
Qy 4233 CGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCAGTCAACAGAAA 4292
Db 361 CGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCAGTCAACAGAAA 420
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Qy 4353 TAACACTGCGGCCCACTTACTTCTGACAAAGATCGGAGGACCGGAGGAGCTTAACCGCTTT 4412
Db 481 TAACACTGCGGCCCACTTACTTCTGACAAAGATCGGAGGACCGGAGGAGCTTAACCGCTTT 540
Qy 4413 TTTTGCAACAATCGGGGATCATCTTAACCTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 4472
Db 541 TTTTGCAACAATCGGGGATCATCTTAACCTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGT 600
Qy 4473 AGCCATACCAAAACGACGAGCGTGAACACAGATGCTGTAGCAATGGCAACAAAGTTGCG 4532
Db 601 AGCCATACCAAAACGACGAGCGTGAACACAGATGCTGTAGCAATGGCAACAAAGTTGCG 660
Qy 4533 CAATCTTAACTGCGGCACTTACTTACTTCTAGCTTCCCGGCAACAAATTAATAGACTGAT 4592
Db 661 CAATCTTAACTGCGGCACTTACTTACTTCTAGCTTCCCGGCAACAAATTAATAGACTGAT 720
Qy 4593 GAGAGCGGATTAAGTTGCGAGGACCACTTCTGCGCTCGGCGCTTCCCGGCTGCTGCTTAT 4652
Db 721 GAGAGCGGATTAAGTTGCGAGGACCACTTCTGCGCTCGGCGCTTCCCGGCTGCTGCTTAT 780
Qy 4653 TGCTGATAATCTGGAGCGCGGTGAGCGTGGGTCTCGCGGTATCAATGACAGCACTGGGGCC 4712
Db 781 TGCTGATAATCTGGAGCGCGGTGAGCGTGGGTCTCGCGGTATCAATGACAGCACTGGGGCC 840
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QY      4713 A 4713
Db      841 A 841

RESULT 9
CD459085
LOCUS   Fg08_08d03_R_Fg08_AAFC_ECORC_Fusarium_graminearum_complex_substrate
DEFINITION
ACCESSION CD459085
VERSION   CD459085.1
KEYWORDS  EST.
SOURCE    Gibberella zeae
ORGANISM  Gibberella zeae

REFERENCE
AUTHORS  Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J.,
          Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
          Spott,D. and Tinker,N.A.
TITLE     A cDNA library prepared from Fusarium graminearum grown on a
          complex plant substrate
JOURNAL  Unpublished (2003)
COMMENT   Contact: Watson, Robert.J.
          Eastern Cereal and Oilseed Research Centre
          Agriculture and Agri-food Canada
          Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
          CANADA
          Tel: (613) 759-1655
          Fax: (613) 759-1701
          Email: watsonrj@agr.gc.ca.

FEATURES
source
1..872
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_08d03"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAFC_ECORC_Fusarium_graminearum_complex_s
ubstrate"
/note="vector: pBluescript II+; Site_1: EcoRI; Site_2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."

ORIGIN
Query Match 14.3%; Score 832.8; DB 14; Length 872;
Best Local Similarity 99.2%; Pred. No. 8.1e-200;
Matches 831; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      3846 TTTTCGGGGAAATGTGCGCGGAACCCCTATTGTTTATTTTCTAAATACATTCACAAATAT
Db      35 TTTTCGGGGAAATGTGCGCGGAACCCCTATTGTTTATTTCTAAATACATTCACAAATAT 94

QY      3906 GTATCCGCTCATGAGACAAATACCTGATTAATGCTTCAATATATTGAAAGGAAGAG
Db      95 GTATCCGCTCATGAGACAAATACCTGATTAATGCTTCAATATATTGAAAGGAAGAG 154

QY      3966 TATGAGTATTCAACATTTTCGTCGCGCCCTATTCCCTTTTTCGGGCATTTTCCTTCC
Db      155 TATGAGTATTCAACATTTTCGTCGCGCCCTATTCCCTTTTTCGGGCATTTTCCTTCC 214

QY      4026 TGTTTTGTCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGC
Db      215 TGTTTTGTCTCACCAGAGAGCGTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGC 274

QY      4086 ACGAGTGGTGTACATCAACCTGATCTCAACAGCGGTGAAGATCCTTCAGAGATTTTCGCC
Db      275 ACGAGTGGTGTACATCAACCTGATCTCAACAGCGGTGAAGATCCTTCAGAGATTTTCGCC 334

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QY      4146 CGAAGAACGTTTTTCCATGATGAGCACATTTTAAAGTTCTGCTATGTGGCGGCTATTATC 4205
Db      335 CGAAGAACGTTTTTCCATGATGAGCACATTTTAAAGTTCTGCTATGTGGCGGCTATTATC 394

QY      4206 CCGTATTGACCGCGGCAAGAGCAACTCGGTGCGGCATACATATTCTCAGAATGACTT 4265
Db      395 CCGTATTGACCGCGGCAAGAGCAACTCGGTGCGGCATACATATTCTCAGAATGACTT 454

QY      4266 GCTTGAGTACTTCACCACTGACAGAAAGCATCTTACCGATGGCATGACAGTAAGGAATT 4325
Db      455 GCTTGAGTACTTCACCACTGACAGAAAGCATCTTACCGATGGCATGACAGTAAGGAATT 514

QY      4326 ATGCAGTGTGCCATACCACTAGTGAATAACACTGCGGCGCAACTTACTTCTGACAAAGAT 4385
Db      515 ATGCAGTGTGCCATACCACTAGTGAATAACACTGCGGCGCAACTTACTTCTGACAAAGAT 574

QY      4386 CGGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAAAACATGGGGGATCANGTAATCTGCGCT 4445
Db      575 CGGAGGACCGAAGGAGCTAAACCGCTTTTTCGCAAAACATGGGGGATCANGTAATCTGCGCT 634

QY      4446 TGATCGTTGGACCGGAGCTGAATGAAGCCATACCAACGAGCGGTGACACCAGAT 4505
Db      635 TGATCGTTGGACCGGAGCTGAATGAAGCCATACCAACGAGCGGTGACACCAGAT 694

QY      4506 GCCTGTAGCAATGCAACAACTGTCGCCAACTATTAACTGCGCAACTTACTTCTCTAGC 4565
Db      595 GCCTGTAGCAATGCAACAACTGTCGCCAACTATTAACTTAACTGCGCAACTTACTTCTCTAGC 754

QY      4566 TTCCCGGCAACAAATTAATAGACTGGATGGAGCGCGGATAAAGTTTCAGAGACCACTTCTCGG 4625
Db      755 TTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTTCAGAGACCACTTCTCGG 814

QY      4626 CTGCGGCTTTCGCGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGG 4683
Db      815 CTGCGGCTTTCGCGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGG 872

RESULT 10
CF269652/c
LOCUS   CF269652
DEFINITION
Fgylcolid844 Fragilariopsis cylindrus SMART cDNA library (Clontech)
Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.
ACCESSION CF269652.1
VERSION   CF269652.1
KEYWORDS  EST.
SOURCE    Fragilariopsis cylindrus
ORGANISM  Fragilariopsis cylindrus
          Bakaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
          Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsids.
          1 (bases 1 to 1073)
          Mock,T. and Valentin,K.
REFERENCE 1..1073
AUTHORS   Mock,T. and Valentin,K.
TITLE     Est analysis of freezing tolerance in the Antarctic diatom
          Fragilariopsis cylindrus: Detection of numerous cold adaption
          related genes and gene transfer events
JOURNAL   Unpublished (2003)
COMMENT   Contact: Mock T
          Biological Oceanography
          Alfred-Wegener-Institute for Polar and Marine Research
          Am Handelshafen 12, D-27570 Bremerhaven, Germany
          Tel: +49 471 4831 1893
          Fax: +49 471 4831 1425
          Email: tmock@awi-bremerhaven.de
          sequence with unknown function
          PCR Primers
          FORWARD: 5'lambdaTriplex2
          BACKWARD: 3'lambdaTriplex2
          Seq primer: ctcgggaagcgcgcattgtgtggt.
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source
1..1073
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/strain="Antarctic"

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Query Match	14.2%;	Score 825;	DB 14;	Length 1073;
Best Local Similarity	96.5%;	Pred. No. 8.1e-198;		
Matches 884;	Conservative 0;	Mismatches 25;	Indels 7;	Gaps 4;
QY	4914	CGTAAATCTCATAGCACAAATCCCTTAAACGTGAGTTTTGTTCCACATGAGCGTCAGACCC	4973	
DB	964	TTATTGTCTCATGCCCAANTCCCTTAAACGTGAGTTTTGTTCCACATGAGCGTCAGACCC	905	
QY	4974	CGTAGAAAAGATCAAAGGATCTTCTTCAGATCTCTTTTTCGCGGTAAATCTGCTGCTT	5033	
DB	904	CGTAGAAAAGATCAAAGGATCTTCTTCAGATCTCTTTTTCGCGGTAAATCTGCTGCTT	845	
QY	5034	GCAACCAAAAACCCACCGCTACACAGCGGTGTTTTGTTCCCGGATCAAGAGCTACCAAC	5093	
DB	844	GCAACCAAAAACCCACCGCTACACAGCGGTGTTTTGTTCCCGGATCAAGAGCTACCAAC	785	
QY	5094	TCCTTTTTCGGAAGGTAACT--GGCTTCAGCAGACGCG-AGATACCAAAATAC-TGTCCTT	5148	
DB	784	TCCTTTTTCGGAAGGTAACT--GGCTTCAGCAGACGCG-AGATACCAAAATAC-TGTCCTT	725	
QY	5149	CTAGTGTAGCG--TAGTTAGGCACACACTTCAAGAACTCTGTAGCACCGCTACATACC	5206	
DB	724	CTAGTGTAGCGNGTAGTTAGNGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACC	665	
QY	5207	TCGCTCTGCTAAATCCTCTGTACAGTGCCTGCTCGCAGTGGCGATAAGTCTGTCTTACCG	5266	
DB	664	TCGCTCTGCTAAATCCTCTGTACAGTGCCTGCTCGCAGTGGCGATAAGTCTGTCTTACCG	605	
QY	5267	GTTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGGAACGGGGGTT	5326	
DB	604	GTTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGGAACGGGGGTT	545	
QY	5327	CGTGCAACAGCCAGCTTCGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTG	5386	
DB	544	CGTGCAACAGCCAGCTTCGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTG	485	
QY	5387	AGCTATGAGAAAAGCCACGCTTCCCGAAGGGAGAAAAGCGGACAGATATCCCGTAAAGCG	5446	
DB	484	AGCTATGAGAAAAGCCACGCTTCCCGAAGGGAGAAAAGCGGACAGATATCCCGTAAAGCG	425	
QY	5447	GCAAGGCTCGNACNAGGAGCGGACGAGGAGCTTCCAGCGGGGNAACGCGTGATCTTT	5506	
DB	424	GCAAGGCTCGNACNAGGAGCGGACGAGGAGCTTCCAGCGGGGNAACGCGTGATCTTT	365	
QY	5507	ATAGTCTCTGTCCGGTTTTCCGCCACTCTGACTTGAAGCGTCGATTTTTCGTGATGCTCGTCAG	5566	
DB	364	ATAGTCTCTGTCCGGTTTTCCGCCACTCTGACTTGAAGCGTCGATTTTTCGTGATGCTCGTCAG	305	
QY	5567	GGGGCGGGAGGCTATATGNAAAAACCCACAGCAAACGCGGCTTTTTCACGGTCTCTGGCCCTTTT	5626	
DB	304	GGGGCGGGAGGCTATATGNAAAAACCCACAGCAAACGCGGCTTTTTCACGGTCTCTGGCCCTTTT	245	
QY	5627	GCTGGCCCTTTTGCTCACAATGTTCTTCTCGCTTATCCCTCGATCTCTGTGATAAACCGTA	5686	
DB	244	GCTGGCCCTTTTGCTCACAATGTTCTTCTCGCTTATCCCTCGATCTCTGTGATAAACCGTA	185	
QY	5687	TTACCGCCCTTTGAGTGAGCTGATACCGCTCCGCGACGCGAACGACCGAGCGCAGCGAGT	5746	
DB	184	TTACCGCCCTTTGAGTGAGCTGATACCGCTCCGCGACGCGAACGACCGAGCGCAGCGAGT	125	

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Db 301 GACAGTAAGAGAAATATGCGAGTGTGCGCATTAACCATGAGTGAATAACTGCGGCCAACTT 360
Qy 4371 ACTTCTGACAAACGATCGGAGGACCGAAGAGCTTAACCGCTTTTGTGCAACATGCGGGA 4430
Db 361 ACTTCTGACAAACGATCGGAGGACCGAA-GAGCTAAACCGCTTTTGTGCAACATGCGGGA 419
Qy 4431 TCATGTAACCTGCGCTTGTATGCTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 4490
Db 420 TCATGTAACCTGCGCTTGTATGCTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 479
Qy 4491 GCGTGACACCAAGATGCTGTAGCAATGGCAACCAACGTTGGCAAACTATTAACTGCGGA 4550
Db 480 GCGTGACACCAAGATGCTGTAGCAATGGCAACCAACGTTGGCAAACTATTAACTGCGGA 539
Qy 4551 ACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGGATGAAGTTGC 4610
Db 540 ACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGGATGAAGTTGC 599
Qy 4611 AGGACCACTTCTGCGCTCGGCCCTTCGGCTGGCTGGCTGTTTATTGCTGATAACTGAGC 4670
Db 600 AGGACCACTTCTGCGCTCGGCCCTTCGGCTGGCTGGCTGTTTATTGCTGATAACTGAGC 659
Qy 4671 CGGTGAGCGTGGTCTCGCGCTATCATTTGACGACACTGGGCGCAGATGTAAGCCCTCCG 4730
Db 660 CGGTGAGCGTGGTCTCGCGCTATCATTTGACGACACTGGGCGCAGATGTAAGCCCTCCG 719
Qy 4731 TATCGTAGTATTATACACGACGGGAGTCAAGCACTATGATGATGAACCAATAGACAGAT 4790
Db 720 TATCGTAGTATTATACACGACGGGAGTCAAGCACTATGATGATGAACCAATAGACAGAT 779
Qy 4791 CGGTGAGATGGTCCCTCACTGATTAAGCAATGATTAAGCAATGATTAAGCAATGATTAAGCA 4850
Db 780 CGGTGAGATGGTCCCTCACTGATTAAGCAATGATTAAGCAATGATTAAGCAATGATTAAGCA 839
Qy 4851 TATACTTTAGATTGA 4865
Db 840 TATGTTGAGATTGA 854
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RESULT 12
CD458333
LOCUS
DEFINITION
  Fg08_09e07_r Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate
  Gibberella zeae cDNA clone Fg08_09e07, mRNA sequence.
CD458333
VERSION
  CD458333.1 GI:31373073
KEYWORDS
  EST.
SOURCE
  Gibberella zeae
  Gibberella zeae
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
  1 (bases 1 to 870)
  Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J.,
  Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
  Sprott,D. and Finkler,N.A.
  A cDNA library prepared from Fusarium graminearum grown on a
  complex plant substrate
  Unpublished (2003)
JOURNAL
  Contact: Watson, Robert J.
  Eastern Cereal and Oilseed Research Centre
  Agriculture and Agri-Food Canada
  Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
  CANADA
  Tel: (613) 759-1655
  Fax: (613) 759-1701
  Email: watsonrj@agr.gc.ca
  Location/Qualifiers
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  /mol_type="mRNA"
  /strain="DAOM 180378"
  /db_xref="taxon:5518"
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/clone="Fg08_09e07"
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XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
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ORIGIN

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Query Match 14.18; Score 819.6; DB 14; Length 870;
Best Local Similarity 99.21; Pred. No. 1.8e-196;
Matches 841; Conservative 3; Mismatches 2; Indels 2; Gaps 2;
Qy 3833 ATACAGGTGGCACTTTTCGGGGAATGTCGCGGAACCCCTATTGTTTATTTTCTAAA 3892
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Qy 3893 TACATTCAAAATATGATCCCTCATGAGACAATTAACCCCTGATAAATGCTTCAATAATT 3952
Db 84 TACATTCAAAATATGATCCCTCATGAGACAATTAACCCCTGATAAATGCTTCAATAATT 143
Qy 3953 GAAAAGGAGATGATGATTTCAACATTTCCGTGCGCCCTATTCCCTTTTTCGGG 4012
Db 144 GAAAAGGAGATGATGATTTCAACATTTCCGTGCGCCCTATTCCCTTTTTCGGG 203
Qy 4013 CATTTTCCTTCTCTGTTTTTCTCACCAGAAACGCTGTGAAAGTAAAGATGCTGAAG 4072
Db 204 CATTTTCCTTCTCTGTTTTTCTCACCAGAAACGCTGTGAAAGTAAAGATGCTGAAG 263
Qy 4073 ATCAGTTGGTGAACGATCGGTTTACATCGAATCGGATCTCAACAGCGGTGAAGATCTTG 4132
Db 264 ATCAGTTGGTGAACGATCGGTTTACATCGAATCGGATCTCAACAGCGGTGAAGATCTTG 323
Qy 4133 AGAGTTTTCGCGCGGAGAAAGCGTTTCCATGATGAGCACTTTTAAAGTTCGTATGTG 4192
Db 324 AGAGTTTTCGCGCGGAGAAAGCGTTTCCATGATGAGCACTTTTAAAGTTCGTATGTG 383
Qy 4193 GCGCGGTATTATCCGTATTGAGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATT 4252
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Db 444 CTGAGATGATCTGTTGATGATCTCAACAGTCAAGAAAGAGCATCTTACGATGCGCATGA 503
Qy 4313 CAGTAAAGAAATTAATGAGTGTGCGCATTAACCATGAGTGAATACACTGCGGCCAACTTAC 4372
Db 504 CAGTAAAGAAATTAATGAGTGTGCGCATTAACCATGAGTGAATACACTGCGGCCAACTTAC 563
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Db 564 TTTCTGACAAACGATCGGAGGACCGAA-GAGCTAAACCGCTTTTTCGCAACATCGGGAT 622
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Qy 4492 CGTGACACCAAGATGCTGTAGCAATGGCAACCAACGTTGGCAAACTATTAACTGCGCAA 4551
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Qy 4552 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGGATGAAGTTGCA 4611
Db 743 CTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGGATGAAGTTGCA 802
Qy 4612 GGACCACTTCTGCGCTCGGCCCTTCGGCTGGCTGGCTGTTTATGCTGATTAATCTGAGCC 4671
Db 803 GGACCACTTCTGCGCTCGGCCCTTCGGCTGGCTGGCTGTTTATGCTGATTAATCTGAGCC 862
Qy 4672 GGTGAGCG 4679
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RESULT 13
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LOCUS    BZ572284.1 1249 bp DNA linear GSS 17-DEC-2002
DEFINITION msh2_2572.x3 msh Pseudomonas aeruginosa genomic clone msh2_2572,
genomic survey sequence.
ACCESSION BZ572284
VERSION   BZ572284.1 GI:27207345
KEYWORDS GSS.
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 1249)
AUTHORS   Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Haetings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE     Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL   J. Bacteriol. (2002) In press
COMMENT   Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES             source
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     1..1249
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     /strain="MSH"
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ORIGIN
Query Match      14.0%; Score 815.6; DB 28; Length 1249;
Best Local Similarity 93.0%; Pred. No. 2e-195;
Matches 952; Conservative 0; Mismatches 61; Indels 11; Gaps 9;
Qy 4799 TAGTGCTCACTGATTAAAGCAATGTAAGTCTGAGCAAGTTTACTCATATATACATT 4858
Db 1116 TATGGGCCCCCATATATAAACACTGGGACCGGACGACCAAGTTTCCCA-AAATACCT 1058
Qy 4859 AGATTGATTAAAACTTCATTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGATA 4918
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Qy 4919 ATCTCATGACCAAAATCCCTTAAAGTGAATTTGTTCCACCTGAGCGTCAGACCCGCTAG 4978
Db 999 ATCTCATG--CCAAATCCCTTACGTGAGTTTTCGTCCCACTAAAGGGCCAGACCCCGTAA 942
Qy 4979 AAAAGATCAAAAGGATCTTTCTTGAGATCCCTTTTCTGCGGTAAATCTGCTGTGCAAA 5038
Db 941 GAAAGAACAAAGATCTTCTGAGAACCTTTTCTGCGGTAAAT-TGCTGCTTGC-AA 884
Qy 5039 CAAAAAACCAACCGCTACAGCGGTGTTGTTGTCGCGATCAAGAGTACCAACTTTT 5098
Db 883 CAAAAAACCAACCGCTACCAACCGTGTGTTG--TTTGGCGATCAAGAGCTA-CAACTCTTT 827
Qy 5099 TTCCGAGGTAACCTGGCTTACGACGAGCGGACATACAAATCTGCTCTCTAGTGTAGC 5158
Db 826 TTCGAGAGGTANCT-GCTTTCAGCAGAGCGGACAGATACAAATCTGTTCTTAGTGTAGC 768
Qy 5159 CGTAGTAGGCCACCACTTCAAGAACTCTGTAGCAACCGCTACATACCTCGCTCTGTCTAA 5218
Db 767 CGTAGTAGGCCACCACTTCAAGAACTCTGTAGCAACCGCTACATACCTCGCTCTGTCTAA 708
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Qy 5219 TCCTGTTACAGTGGCTGCTGCGCAGTGGCGATAAGTCTGTGTTTACCGGTTGGACTCAA 5278
Db 707 TCCTGTTACAGTGGCTGCTGCGCAGTGGCGATAAGTCTGTGTTTACCGGTTGGACTCAA 648
Qy 5279 GACGATAGTATCCGATTAAGCGCGAGCGCTGGGCTGAAACGGGGGTTTCGTGCACACAGC 5338
Db 647 GACGATAGTATCCGATTAAGCGCGAGCGCTGGGCTGAAACGGGGGTTTCGTGCACACAGC 588
Qy 5339 CCAGCTTCGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAA 5398
Db 587 CCAGCTTCGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAA 528
Qy 5399 GGGCCACGCTTCCCGAAGCGGAGAAAGCGGACAGATATCCGTAAGCGGACGGTCCGAA 5458
Db 527 GGGCCACGCTTCCCGAAGCGGAGAAAGCGGACAGATATCCGTAAGCGGACGGTCCGAA 468
Qy 5459 CAGGAGAGCGACGAGGAGGAGCTTCCAGGGGGAACCGCTGTATCTTTATAGTCTGTGCG 5518
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Qy 5519 GGTTCGCGCAGCTCTGACTTGAGCGTTCGATTTTGTGATGCTGTCAGGGGCGGAGCC 5578
Db 407 GGTTCGCGCAGCTCTGACTTGAGCGTTCGATTTTGTGATGCTGTCAGGGGCGGAGCC 348
Qy 5579 TATGCAAAAACGCCAGCAACGGGCGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTG 5638
Db 347 TATGCAAAAACGCCAGCAACGGGCGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTG 288
Qy 5639 CTCACATGTTCTTCTGCTGCTTATCCCTGATTTCTGTGATAAACCGTATTACCGCTTTG 5698
Db 287 CTCACATGTTCTTCTGCTGCTTATCCCTGATTTCTGTGATAAACCGTATTACCGCTTTG 228
Qy 5699 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACGAGCGGACGAGTCAGTGAGGAGG 5758
Db 227 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACGAGCGGACGAGTCAGTGAGGAGG 168
Qy 5759 AAGCGGAGAGCGGCCAATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTAAT 5818
Db 167 AAGCGGAGAGCGGCCAATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTAAT 108
Qy 5819 GCAG 5822
Db 107 GCAG 104
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RESULT 14
BZ577702
LOCUS BZ577702 1126 bp DNA linear GSS 17-DEC-2002
DEFINITION msh2_5533.y2 msh Pseudomonas aeruginosa genomic clone msh2_5533,
genomic survey sequence.
ACCESSION BZ577702
VERSION BZ577702.1 GI:27212763
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 1126)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Haetings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES Location/Qualifiers

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/mol_type="genomic DNA"
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/note="Environmental isolate. Whole genomic shotgun
library."

ORIGIN
Query Match 14.0%; Score 814.4; DB 28; Length 1126;
Best Local Similarity 90.4%; Pred. No. 4e-195;
Matches 938; Conservative 0; Mismatches 91; Indels 9; Gaps 6;

Qy 3881 TATTTTTCTAAATACATTCAAATATGATCGCTCATGAGACAAATAACCCCTGATAAATGC 3940
Db 93 TATTTTTCTAAATACATTCAAATATGATCGCTCATGAGACAAATAACCCCTGATAAATGC 152

Qy 3941 TTCAATAATATTGMAAAGGAAGATGATGAGTATTCAACATTTCCGTGTGCGCCCTTATTC 4000
Db 153 TTCAATAATATTGMAAAGGAAGATGATGAGTATTCAACATTTCCGTGTGCGCCCTTATTC 212

Qy 4001 CCTTTTTGCGGCATTTTGGCTTCTGCTTTTGTGCTCAACCAGAAAACGCTGCTGAAGTAA 4060
Db 213 CCTTTTTGCGGCATTTTGGCTTCTGCTTTTGTCTACCCAGAAAACGCTGCTGAAGTAA 272

Qy 4061 AAGATGCTGAAGATCAGTTCGGTGCAAGAGTGGGTATCATTCGAATCTCGATCTCAACAGCG 4120
Db 273 AAGATGCTGAAGATCAGTTCGGTGCAAGAGTGGGTATCATTCGAATCTCGATCTCAACAGCG 332

Qy 4121 GTAAGATCCTTTGAGAGTTTTCGCCCCCGAAGAACGTTTTTCCAATGATCAGACACTTTTAAAG 4180
Db 333 GTAAGATCCTTTGAGAGTTTTCGCCCCCGAAGAACGTTTTTCCAATGATCAGACACTTTTAAAG 392

Qy 4181 TTCGTCTATGTGGCGCGGTATTAATCCCGTATTTGACGCGCGGCAAGACAACTCGGTGCGC 4240
Db 393 TTCGTCTATGTGGCGCGGTATTAATCCCGTATTTGACGCGCGGCAAGACAACTCGGTGCGC 452

Qy 4241 GCATACACTATTCTCAGAAAGACTTGTGCTGAGTACTCACCAAGTACACAGAAAGCATCTTA 4300
Db 453 GCATACACTATTCTCAGAAAGACTTGTGCTGAGTACTCACCAAGTACACAGAAAGCATCTTA 512

Qy 4301 CGGATGCGATGACAGTAAGAAATTAATGCAAGTGTGCGCATAAACATGAGTGAATAACAATG 4360
Db 513 CGGATGCGATGACAGTAAGAAATTAATGCAAGTGTGCGCATAAACATGAGTGAATAACAATG 572

Qy 4361 CGGCAACTTACTTCTGACAAAGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTTGTGCACA 4420
Db 573 CGGTCAACTTACTTATGACAAAGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTTGTGCACA 632

Qy 4421 ACATGGGGATCATGTAACCTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGACCATAC 4480
Db 633 ACATGGCGGATCATGTAACCTCGCTTGATCGTTGGGAACCGGAGCTGAATGAAGACCATAC 692

Qy 4481 CAAACGACGAGCGTGACACCAACGATGCTGTAGCAATGGCAACAAACGTCGCGCAAACTAT 4540
Db 693 CAAACGACGAGCGTGACACCAACGATGCTGTAGCAATGGCAACAAACGTCGCGCAACTAT 752

Qy 4541 TAACTGCGCAACTATTACTTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGCGG 4600
Db 753 TAACTGCGCAACTACTGACTCTAGCTTTCGCGGACACAAATAATAGACTGGATGGAGCGG 812

Qy 4601 AT-AAAAGTTCAGGACCACTTCTGCGCTCGGCCCTTCGCGCTGGCTGGTTTATGCTGAT 4659
Db 813 ATAAAAGTTCAGGACCACTTTTGGGCTCGGCCCTTTCGGATGGCTTATTTGGTGA 872

Qy 4660 AAATCTCGAGCGGTGAGCGTGGGTCTCGCGGTATCAATTCGACACTGGGGCGCAGATGGT 4719
Db 873 TAAATTGAGCGCGGGGAACGGGGGGCTCGCGGTTACATTCGCACTACTTGGGGCAATAGG 932

Qy 4720 AAGCCCTCCGCTATCGTAGTTATCTACACGA-CGGGGAGTCAGGCAACTA-TGGATGAAC 4777

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Db      ||||| 241 TCTCAGAAATGACTTGGTTGAGTACTCACCAGTCAAGAAAAGCATCTTACGGATGGCATG 300
Qy      ||||| 4312 ACAGTAAGAGAAATTATGCGAGTGTGCGCATACCATGAGTGTGATAACA CTGCGGCCAACTTA 4371
Db      ||||| 301 ACAGTAAGAGAAATTATGCGAGTGTGCGCATACCATGAGTGTGATAACA CTGCGGCCAACTTA 360
Qy      ||||| 4372 CTTCTGACAAAGATCGGAGGACCCGAAGAGCTAACCGCTTTTGTGCAACAATGGGGAT 4431
Db      ||||| 361 CTTCTGACAAAGATCGGAGGACCCGAA -GAGCTAACCGCTTTTGTGCAACAATGGGGAT 419
Qy      ||||| 4432 CATCTRACTGCGCTTGATCGTTGGGACCGGAGCTGATGAGCCATACCAAAACGAGAG 4491
Db      ||||| 420 CATGTAACTGCGCTTGATCGTTGGGACCGGAGCTGAATGAAGCCATACCAAAACGAGAG 479
Qy      ||||| 4492 CGTGACACACGATGCGCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAA 4551
Db      ||||| 480 CGTGACACACGATGCGCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAA 539
Qy      ||||| 4552 CTACTTACTCTAGCTTCCCGGCAACAATTAAATAGACTGGATGGAGCGGATAAAGTTGCA 4611
Db      ||||| 540 CTACTTACTCTAGCTTCCCGGCAACAATTAAATAGACTGGATGGAGCGGATAAAGTTGCA 599
Qy      ||||| 4612 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCC 4671
Db      ||||| 600 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCC 659
Qy      ||||| 4672 GGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCATCTGGGGCCAGATGGTAAGCCCTCCCGT 4731
Db      ||||| 660 GGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCATCTGGGGCCAGATGGTAAGCCCTCCCGT 719
Qy      ||||| 4732 ATCGTAGTTATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATC 4791
Db      ||||| 720 ATCGTAGTTATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATC 779
Qy      ||||| 4792 GCTGAGATAGTGTGCTCACTGATTTAAGCATTTGGTAACGT 4831
Db      ||||| 780 GCTGAGATAGTGTGCTCACTGATTTAAGCATTTGGTAACGT 819
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Job time : 13315 secs